Basidiomycota isolated from the Mediterranean Sea – Phylogeny and putative ecological roles

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Running Head: Basidiomycota in marine environment

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Abstract

Basidiomycota are an ecologically and taxonomically diverse fungal phylum, colonizing all terrestrial ecosystems, with 30,000 described species. By contrast, in marine habitats Basidiomycota are under-represented when compared to the more abundant Ascomycota. Recently, we investigated the marine mycobiota mainly in the Mediterranean Sea, confirming the scarcity of Basidiomycota. However, a low rank taxonomic identification based on morphological features, proved impossible, since most of the strains remained sterile in axenic culture. Nevertheless, considering the great potential and biotechnological value of Basidiomycota, it would be useful to define their precise taxonomic placement. To this end, 34 marine Basidiomycota isolated from different marine substrates underwent molecular analyses and 123 newly generated sequences were obtained and deposited in GenBank.

Sequencing of the Internal Transcribed Spacer (nrITS) regions allowed us to affiliate the 34 strains with six classes, but a lower taxonomic identification was reached with a multi-locus phylogenetic analysis.

Keywords: Marine fungi; Algae; Sponges; Phylogeny; Bioremediation; Biotechnological potential

1. Introduction

The marine environment, commonly divided into coastal regions (influenced by land), pelagic and deep-sea habitats (recognised as extreme), is home to a huge variety of microorganisms, among which fungi are often dominant (Richards et al., 2012). Marine fungi are classified as obligate that grow and reproduce exclusively in the sea, or facultative, terrestrial species able to grow and reproduce in marine environments. Those fungi whose obligate or facultative marine nature is undefined are called marine-derived. Marine fungi have been retrieved worldwide from a broad range of biotic and abiotic substrates such as algae, sponges, corals, sediments etc. (Jones and Pang, 2012; Raghukumar, 2017). Living as mutualists (ecto- and endosymbionts), parasites, pathogens and saprobes, these organisms play an important role as primary degraders, thus contributing to nutrient recycling (Raghukumar, 2017; Richards et al., 2012). Even if the total number of marine fungi has been estimated to exceed 10,000 taxa, a recent update on accepted classification described only 1,112 species, mostly affiliated to Ascomycota (Jones et al., 2015). Basidiomycota are under-represented, with only 74 species (12 obligate and 62 facultative) contributing to marine fungal diversity (Jones et al., 2015; Jones and Pang, 2012; Raghukumar, 2017).

Basidiomycota living in marine habitats are an ecologically and taxonomically diverse group morphologically categorised as filamentous species, able to grow on several substrates such as seagrasses and mangrove wood, and single-celled yeasts, found in association with algae, seagrasses and dead animals or free-floating in the sea. In addition, some fungi (e.g. Cystobasidiales) can exhibit true dimorphism (Jones and Pang, 2012). Most of the Basidiomycota retrieved from the above mentioned unique environments belong to the following classes: Agaricomycetes (e.g. *Nia vibrissa* and *Schizophyllum commune, Grammothele fuligo, Peniophora* sp.), Microbotryomycetes (e.g. *Rhodosporidium diobovantum* and *R. babjeave*), Tremellomycetes (e.g. *Cryptococcus* spp.), Ustilaginomycetes (e.g. *Pseudozyma aphidis*), and Wallemiomycetes (e.g. *Wallemia sebi*) (Jones et al., 2015). Yet, a significant number of taxa remain undescribed or identified only at genus level. This

is mainly due to the following reasons: i) several isolates in axenic cultures do not develop the reproductive structures necessary for morphological identification (sterile mycelia) (Bovio et al., 2017; Gnavi et al., 2017; Panno et al., 2013); ii) molecular approaches relying on the internal transcribed spacers (nrITS), small or large ribosomal subunits (nrSSU and nrLSU) are not always exhaustive (Binder et al., 2013; Hibbett et al., 2014; Hibbett et al., 2007; Jancic et al., 2015).

Among marine fungi, the understudied Basidiomycota may be an untapped source of potentially novel enzymes and bioactive compounds due to the extreme environmental conditions they adapt to (high salinity and pressure, pH, oxidative stress, low temperature, chemicals and metals) (Bodke et al., 2012; Dalmaso et al., 2015). For instance, the production of ligninolytic enzymes, such as peroxidases and laccases, is well documented in the sponge derived strain *Peniophora* sp. CBMAI 1063 (Bonugli-Santos et al., 2012; Bonugli-Santos et al., 2016), in the mangrove associated *Phlebia* sp. MG-60 (Luo et al., 2005; Raghukumar et al., 2008) and in *Flavodon flavus* isolated from the seagrass *Thalassia hemprichii* (Mtui and Nakamura, 2008). This could signal the great potential of salt-tolerant Basidiomycota in treating coloured industrial effluents and in degrading aromatic recalcitrant pollutants (Bonugli-Santos et al., 2012).

Recently, the cultivable mycobiota associated to macro-algae, seagrasses, sponges and a crude oil contaminated site were investigated in the Mediterranean Sea and in the Atlantic Ocean, confirming the scarcity of Basidiomycota in comparison to their terrestrial counterpart and to the most dominant Ascomycota (Bovio et al., 2017; Garzoli et al., 2015; Gnavi et al., 2017; Panno et al., 2013). In this paper, by means of a combined multi-locus phylogenetic analysis, the authors provide a better phylogenetic placement of 34 Basidiomycota (Bovio et al., 2017; Gnavi et al., 2017; Panno et al., 2013), thus increasing our understanding of fungal diversity in the marine environment.

2. Materials and Methods

2.1. Fungal isolates and DNA extraction.

Fungal isolates used in this study were previously retrieved from different substrates in the Mediterranean Sea and in the Atlantic Ocean (Table 1) and are preserved at the *Mycotheca Universitatis Taurinensis* (MUT). The organisms were originally isolated on Corn Meal Agar SeaWater (CMASW; SW, 3.4% w/v Sea Salt mix – Sigma-Aldrich, Saint Louis, USA – in ddH_2O) medium.

Genomic DNA was extracted from about 100 mg of mycelium, which was carefully scraped from Malt Extract Agar (MEA) plates, transferred to a 2 mL Eppendorf tubes and disrupted in a MM400 tissue lyzer (Retsch GmbH, Haan, Germany). A NucleoSpin kit (Macherey Nagel GmbH, Duren, DE, USA) was used and extraction proceeded according to the manufacturer's instructions. The quality and quantity of DNA samples were measured spectrophotometrically with Infinite 200 PRO NanoQuant (TECAN, Switzerland). DNA was stored at -20° C.

2.2. PCR amplification and data assembling

Depending on the order/family of affiliation and on the availability of sequences in GenBank, specific markers were amplified in a T100 Thermal Cycler (Bio-Rad, Hercules, CA, USA) (Hibbett et al., 2007).

The nrITS rDNA region was amplified for all strains using the universal primers ITS1/ITS4 (White et al., 1990). Partial nrLSU rDNA was amplified for Polyporales, Psathyrellaceae and Schizophyllaceae using the universal primers LROR/LR7 (Vilgalys and Hester, 1990); partial nrSSU rDNA for Ustilaginaceae, Cistobasidiomycetes, Microbotriomycetes and Holtermanniales using primers PNS1/NS41 (Hibbett, 1996); D1/D2 region of nrLSU rDNA for Ustilaginaceae, Cistobasidiomycetes, Microbotriomycetes and Holtermanniales using primers NL1/NL4 (Kurtzman

and Robnett, 1998). The thermocycler was programmed as previously described (Gnavi et al., 2017; Kurtzman and Robnett, 1998).

For Wallemiaceae, partial sequences of the protein coding genes RNA polymerase II subunits *rpb1* and *rpb2* were obtained by using primers RPB1WF/RPB1WR and RPB2WF/RPB2WR, respectively (Nguyen et al., 2015); RPB1-Af/RPB1-Cr were used to amplify *rpb1* in Polyporales and Psathyrellaceae (Carlson et al., 2014; Matheny, 2005). Translation elongation factor *ef-1α* was amplified by using primers EFdf/EF1-2218R (Matheny et al., 2007) for Cistobasidiomycetes, Microbotriomycetes, Schizophyllaceae, Holtermanniales, Psathyrellaceae and Polyporales. Finally, partial sequences of the pre-rRNA processing protein encoding gene *tsr1* were amplified for the Wallemiaceae with the specific primer pair TSR1WF/TSR1WR (Nguyen et al., 2015). PCR parameters for *rpb1* were: initial denaturation at 95 °C for 3 min; 36 cycles at 95 °C for 30 s, 50 °C for 1 min and 72 °C for 1 min; final extension of 8 min at 72 °C. A touchdown PCR protocol was set for *ef-1α* gene: initial denaturation at 94 °C for 2 min; 9 cycles at 94 °C for 40 s, 60 °C for 40 s (minus 1°C per cycle), 72 °C for 2 min; 36 cycles at 94 °C for 45 s, annealing at 53 °C for 1 min 30 s, extension at 72 °C for 2 min; final extension at 72 °C for 10 min. The PCR profile for *rpb1W*, *rpb2W* and *tsr1W* was as described in Nguyern at al. (2015).

Reaction mixture consisted of 20 ng genomic DNA**,** 10x PCR Buffer (15 mM $MgCl_2$,500 mM KCl, 100 mM Tris-HCl, pH 8.3), 200 µM each dNTP, 1 µM each primer, 2.5 U Taq DNA Polymerase (Qiagen, Chatsworth, CA, USA), in 50 µL final volume. For problematic cases, additional $MgCl_2$ and/or 2.5% DMSO facilitated the reaction.

Amplicons were visualized on a 1.5 % agarose gel stained with 5 mL 100 mL^{-1} ethidium bromide and a GelPilot 1 kb plus DNA Ladder was used; PCR products were purified and sequenced at Macrogen Europe Laboratory (Amsterdam, The Netherlands). The resulting ABI chromatograms were processed and assembled to obtain consensus sequences using Sequencer 5.0 (GeneCodes, Ann

Arbor, Michigan, USA http://www.genecodes.com). Newly generated sequences were deposited in GenBank (Table 1).

2.3. Sequence alignment and phylogenetic analysis

Eleven datasets were assembled on the basis of BLASTn results and of recent phylogenetic studies that included allied taxa, as follows: Psathyrellaceae (Nagy et al., 2013; Orstadius et al., 2015), Peniophoraceae (Hallenberg et al., 1996), Ustilaginaceae (Wang et al., 2015a), Sporidiobolaceae (Wang et al., 2015b), Schizophyllaceae (Siqueira et al., 2016), Polyporales (Phleboid clade and *Trametes*) (Binder et al., 2013; Justo and Hibbett, 2011; Miettinen et al., 2016), Holtermanniales (Liu et al., 2015; Wuczkowski et al., 2011) and Wallemiales (Jancic et al., 2015) (Table 2; Table S1-S9). Sequences were retrieved from GenBank.

Alignments for each gene were generated using MUSCLE (default conditions for gap openings and gap extension penalties), implemented in MEGA v. 7.0 (Molecular Evolutionary Genetics Analysis), visually inspected and trimmed by TrimAl v. 1.2 (http://trimal.cgenomics.org) to delimit and discard ambiguously aligned regions. Since preliminary analyses suggested no incongruence among single-loci phylogenetic trees, alignments were concatenated into a single data matrix with SequenceMatrix v. 1.8 (Vaidya et al., 2011). The appropriate evolutionary model under the Akaike Information Criterion (AIC) was determined for each partition with jModelTest 2 (Darriba et al., 2012). Phylogenetic inferences were calculated using two approaches. First, Bayesian Inference (BI) was performed with MrBayes 3.2.2 (Ronquist et al., 2012) under GTR + I + G evolutionary model (best model). The alignment was run for 10 million generations with two independent runs each containing four Markov Chains Monte Carlo (MCMC) and sampling every 1000 iterations. The first 2,500 trees were discarded as "burn-in" (25 %). Using the Sumt function of MrBayes a consensus tree was generated and Bayesian posterior probabilities (BPP) were estimated. In a second approach, Maximum Likelihood (ML) estimate was performed using RAxML v. 8.1.2 (Stamatakis, 2014) with the same substitution model (GTR + G + I) and 1,000 boostrap replicates. Support values from

bootstrapping runs (MLB) were mapped on the globally best tree using the "-f a" option of RAxML and "-x 12345" as a random seed to invoke the novel rapid bootstrapping algorithm.

Consensus trees were imported and visualized in FigTree v. 1.4.2 (http://tree.bio.ed.ac.uk/software/figtree). Due to the topological similarity similarity of the two resulting trees, only Bayesian analysis with BPP values are reported (Figures 1-9).

3. Results and Discussion

Thirty-four Basidiomycota retrieved from a range of marine substrates were previously identified at genus, family, order and sometimes at class level, on the basis of a single ribosomal gene (nrITS or 26S) (Bovio et al., 2017; Gnavi et al., 2017; Panno et al., 2013). However, the nrITS marker is not sufficient for a thorough phylogenetic analyses, due to intraspecies (across a population of individuals) and intra-genomic (due to multiple copies of the ribosomal region distributed over one or more chromosomal locations) variations (Lindner and Banik, 2011). Protein-coding genes such as *ef-1α*, *rpb1* and *rpb2* are more suitable for a deep phylogeny, since a high variability in the intronic regions is combined with more conserved exons (Raja et al., 2017; Stielow et al., 2015). To identify the strains under investigation (Table 2) at lower taxonomic levels, appropriate molecular markers were amplified. Unfortunately, due to the lack of sequences in public databases, it was not always possible to build complete datasets. The family Peniophoraceae (Russulales) was an extreme case and only an nrITS - based dataset was created (Table S.3). Amplification of *rpb1* and *rpb2* was often problematic, and valid sequences were obtained only for the order Wallemiales by using specific non-degenerated primers. In total, 123 newly generated sequences were obtained: 29 nrITS, 31 nrLSU, 8 nrSSU, 6 D1/D2, 33 *ef-1α*, 13 *rpb1*, 2 *rpb2* and 2 *tsr1* (Table1).

By applying a multi-locus approach, species identification was achieved for twenty Agaricomycetes (Fig. 1, 2, 3, 4, 5, S.1, S.2), one Cystobasiodiomycetes (Fig. 6), five Microbotriomytcetes (Fig. 6), one Tremellomycetes (Fig. S.3), one Ustilaginomycetes (Fig. S.4), and two Wallemiomycetes (Fig. 7). Four strains were identified only at genus level (Fig. 1).

3.1. Agaricomycetes

Agaricomycetes are widely distributed in the marine environment and have been commonly recovered from mangroves (Jones and Pang, 2012), sponges (Gao et al., 2008; Naim et al., 2017) and deep-sea sediments (Zhang et al., 2016). According to nrITS similarity, 24 Agaricomycetes were classified as Agaricales (14), Polyporales (8) and Russulales (2).

3.1.1. Agaricales

Within this order, six strains belonged to Psathyrellaceae and eight to Schizophyllaceae. For both families, consensus phylogenetic trees were based on nrITS, nrLSU and *ef-1α* (Fig. 1, 2). The strain MUT 4775 was identified as *Coprinellus radians* and MUT 2331 as *Psathyrella candolleana*. The species *C. radians* is not new to the marine environment and was found in association with the marine sponge *Dragmacidon reticulatum* (Passarini et al., 2015) and with the zoanthid *Palythoa haddoni* (Qin et al., 2015). Species of *Psathyrella* occur mainly in terrestrial habitats, even though the ability to occupy uncommon niches is not rare for this genus (e.g. *P. aquatica* produces basidiomes underwater in the Rogue River in Oregon) (Frank et al., 2010). For MUT 2232, MUT 2282, MUT 4897 and MUT 5171 it was not possible to go below genus level (Fig.1), but a focus on the genus *Coprinellus* placed MUT 4897 and MUT 5171 within the "bisporus" group of the core Setulosi clade, and MUT 2232 and MUT 2282 in the Micacei clade (Fig. S.1). Although the presence of new lineages cannot be excluded, it would be risky to claim a novel species, since the lack of *ef-1α* reference sequences in GenBank is an issue that must be taken into account.

With respect to Schizophyllaceae, two clades of *Schizophyllum commune* were recognised (Fig. 2), and the strains of marine origin fell into clade 1. To ensure the validity of our findings, three strains of terrestrial *S. commune* (MUT 1037, MUT 3331 and MUT 3335) were included in the analysis. The isolates under investigation were confirmed to be *S. commune* (Fig. 2), an organism that has been often found in marine environments (Gnavi et al., 2017; Liu et al., 2017; Zhang et al., 2016; Joel and Bhimba, 2013; Panno et al., 2013; Gao et al., 2008). With the exception of MUT 3019, all the strains

were isolated from algae and seagrass, whose colonization may be facilitated by the secretion of the hemicellulose degrading xylanases (Kolenova et al., 2005; Rytioja et al., 2014). In fact, MUT 4875 and MUT 5240 were seen to use xylan as the sole source of carbon in the presence of salt (personal communication by Drs Spina and Garzoli).

3.1.2. Russulales

Due to the lack of sequences in public databases, the phylogenetic tree relative to the order Russulales (family Peniophoraceae) was based only on nrITS. Regardless of this, MUT 4993 and MUT 5203 were recognised as *Peniophora cinerea* and *P. incarnata*, respectively. Unidentified strains of *Peniophora* were isolated from the tropical seagrass *Enhalus acoroides* (Sakayaroj et al., 2010), sediments (González-Martínez et al., 2017) and from the Brazilian sponge *Amphimedon viridis* (Menezes et al., 2010).

Lee et al. (2014) accepted *P. cinerea* and *P. incarnata* as highly efficient degraders of polycyclic hydrocarbons. Intriguingly, two strains of *Peniophora* sp. were retrieved from an oil polluted marine site in the Mediterranean sea (Bovio et al., 2017).

3.1.3 Polyporales

Eight isolates belonged to four families of the order Polyporales, namely Bjerkanderaceae (MUT 2492 and MUT 5195), Irpicaceae (MUT 2288, MUT 2370 and MUT 2966), Meruliaceae (MUT 1939) and Polyporaceae (MUT 2444 and MUT 3263). Bjerkanderaceae, Irpicaceae and Meruliaceae were part of the Phleboid clade (plus *Tyromyces* clade) of Polyporales (Binder et al., 2013). A three loci dataset (nrITS, nrLSU and *ef-1α*) was created to build a consensus phylogenetic tree (Fig. 4). MUT 2370 and MUT 2966 formed a strongly supported cluster with *Irpex lacteus*, while MUT 2288 grouped with *Ceriporia lacerata*, two species that have recently been detected in deep-sea sediments (Liu et al., 2017; Zhang et al., 2016).

MUT 5195 clustered together with *Bjerkandera adusta*. MUT 2492 appeared related to *Lopharia spadicea*, although affiliation to other species could not be excluded. To further knowledge of this issue, herbarium specimens of *Porostereum fulvum* were obtained from the Université Claude Bernard, Lyon (LY18491 and LY18496; Table 1) and a focus on the Bjerkanderaceae was based on a two-loci dataset (nrITS and nrLSU) (Fig S.2). As a result, MUT 2492 was identified as *L. spadicea*. This organism may play an important role in the marine ecosystem: beside the ability to reduce wastewater toxicity (Tigini et al., 2013), *L. spadicea* exhibits algicidal properties (Jia et al., 2013). Finally, MUT 1939, isolated from polluted seawater in the Mediterranean Sea (Bovio et al., 2017), was identified as *Tyromyces fissilis*, found for the first time in the marine habitat.

As for Polyporaceae, MUT 2444 and MUT 3263 were at first recognised as *Trametes* sp. Following a phylogenetic analysis focused on the genus *Trametes* and based on a five-loci dataset (nrITS, nrLSU, *rpb1*, *rpb2*, *ef-1α*), the two isolates were identified as *T. gibbosa* (Lenzites clade) (Fig. 5), a species that had never been found in any marine habitats until now. The ability of species of *Trametes* to degrade PAH, and pentahlorophenols (PCP) through lignocellulolytic enzymes is widely accepted (Treu and Falandysz, 2017). Moreover, Knezevic et al. (2015) assessed the protective activity of *T. gibbosa* extracts against H_2O_2-induced DNA damage in human peripheral blood leukocytes. Finally, methanol extracts of *T. gibbosa* showed a broad spectrum of activity against a number of pathogens such as *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* etc. (Appiah et al., 2017). Beside a degradative function, these evidences may indicate a protective role against pathogens and/or damage caused to the sponges by potential mutagenic compounds.

3.2. Cystobasidiomycetes and Microbotryomycetes

According to the D1/D2 region of nrLSU, one strain was associated to Cystobasidiomycetes (order *incertae sedis*) and five to Microbotryomycetes (order Sporidiobolales). A four-loci (nrSSU, nrITS, D1/D2, *ef-1α*) dataset was created and identification at species level was reached for all isolates (Table S.6, Fig. 6).

3.2.1. Cystobasidiomycetes *incertae sedis*

Among Cystobasidiomycetes (Fig. 6), MUT 5471 isolated from *P. pavonica*, fell into the Aurantiaca clade of the Buckleyzymaceae family proposed by Wang et al. (2015b) and was identified as *Buckleyzyma aurantiaca*, a psychrophilic yeast frequently found in cold habitats and in deep-sea sediments (Nagahama et al., 2001; Sabri et al., 2001). Noteworthy is the ability of this organism to produce antioxidant and photoprotective carotenoids (Zoz et al., 2015) that, besides being of biotechnological importance, could guarantee adaptation advantages in the sea.

3.2.2. Sporidiobolales

The order Sporidiobolales consists of three separate clades: *Rhodosporidium*, *Sporidiobolus* and mixed *Rhodosporidium/Sporidiobolus* (Wang et al., 2015b). These basidiomycetous yeasts are common inhabitants of the marine habitats and have been frequently found in deep-sea waters (Raghukumar, 2017). MUT 73, MUT 2266, MUT 2415 and MUT 2669 belonged to the *Rhodosporidium* clade, whereas MUT 4384 fell into the *Sporidiobolus* group (Fig. 6). Specifically, MUT 2266 and MUT 73 were recognised as *Rhodotorula graminis* while MUT 2669 was identified as *R. diobovata*. MUT 2415 formed a mixed cluster together with *R. mucilaginosa*, *R. pacifica*, *R. sphaerocarpa* and *R. taiwanensis*; however, Blastn analysis of two markers (nrITS and D1/D2) showed a 100% similarity with strains of *R. mucilaginosa*. Finally, MUT 4384 was identified as *Sporobolomyces roseus*. The role of yeast cells in the sea is still unclear although a positive correlation between their density and water pollution has been demonstrated long ago (Hagler and Mendonça-Hagler, 1981). Strains of *R. diobovata* and *R. mucilaginosa* have been found in the sea surface microlayer, where levels of UV and concentrations of pollutants are particularly high (Chang et al., 2016). Moreover, Wang et al. (2016), showed the ability of a marine strain of *R. mucilaginosa* (Mar-Y3) to degrade dimethyl phthalate esters (DMPE), used in plastic products, cosmetics and insecticides. A recent investigation reported high concentrations of phthalate esters in coastal areas near Marseilles indicating an excess of these compounds throughout the Mediterranean (Paluselli et

al., 2017), which would justify the presence of *R. mucilaginosa* MUT 2415 on the sponge *G. compressa*.

3.3. Tremellomycetes and Ustilagomycetes

Only two strains (MUT 2943 and MUT 2264), isolated from two Atlantic sponges, were affiliated with Tremellomycetes and Ustilagomycetes.

3.3.1 Holtermanniales

MUT 2943 belonged to the Holtermanniales, a small order of the class Tremellomycetes that includes extremophilic yeasts commonly found in the Arctic, Antarctic, Alpine environments and salty lakes (Turchetti et al., 2013; Wuczkowski et al., 2011; Zhang et al., 2017). Taxonomic assignment was inferred by building a four-loci (nrITS, nrSSU, D1/D2, *ef-1α*) phylogenetic tree (Fig. 7). MUT 2943 grouped into the *Holtermanniella festucosa* clade, a species found in association with the Arctic sponge *Halichondria panicea* (Kachalkin, 2014), but never in seawater in temperate regions. By investigating a strain of *H. festucosa* isolated from an oligotrophic lake in Patagonia, Brandao et al. (2011) observed pectinolytic and esterase activities and production of mycosporine, a UV-absorbing metabolite. This makes MUT 2943 fascinating from at least two points of view: beside a potential application in cosmeceutical, it might shield its host from microbial biofilm formation (Masak et al., 2014; Orgaz et al., 2006).

3.4.2. Ustilaginales

Ustilaginales and Urocystales are the two orders recognised in the class Ustilaginomycetes (Wang et al., 2015a). MUT 2264 fell into the Moesziomyces group of the Ustilaginaceae (Ustilaginales), together with *Pseudozyma aphidis* (currently *Moesziomyces aphidis*) and *P. rugulosa* (Fig. 8). Considering the high similarity (99%) of nrITS, nrSSU and D1/D2 with sequences available in GenBank, this strain was identified as *P. aphidis*, which has been recently hypothesised to be conspecific with *P. rugulosa* (Kruse et al., 2017). In 2003, Gadanho et al. isolated this yeast from

water samples collected in the Atlantic Ocean (south Portugal). Furthermore, two excellent squalene producers, *Pseudozyma* sp. JCC207 and *Pseudozyma* sp. SD301, were found in seawater (100 m below the surface) (Chang et al., 2008) and in the mangrove ecosystem (seawater and soil) (Song et al., 2015). The synthesis of squalene, sought for pharmaceutical applications due to its antimicrobial, antitumor and antioxidant properties, increases significantly in *Pseudozyma* sp. SD301 at 1.5% and 3% sea salt concentrations (Song et al., 2015). Last, but not the least, *P. aphidis* is a great producer of biosurfactants (Goossens et al., 2016), molecules important in the degradation of hydrophobic contaminants. Considering the salinity of the Atlantic Ocean (around 3%) and the great volumes of seawater filtered daily by sponges, *P. aphidis* MUT 2264 may protect its host from both biotic and abiotic dangers.

3.4. Wallemiomycetes

Wallemiomycetes, consists of the single order Wallemiales and the single monogeneric family Wallemiaceae. On the basis of nrITS region, MUT 103 and MUT 4935 were highly similar (>98%) to members of the *Wallemia sebi* species complex (WSSC), which includes *W. canadiensis*, *W. mellicola*, *W. sebi* and *W. tropicalis* (Jancic et al., 2015). Specific primers developed by Nguyen et al. (2015) were used to amplify the protein coding genes *tsr1*, *rpb1* and *rpb2*; the consensus phylogenetic tree (Fig. 7) allowed to identify the two organisms as *W. sebi sensu strictu*. Living in harsh environments such as hypersaline water (Zalar et al., 2005), *W. sebi* is recognised as xerophilic and halotolerant. MUT 103 and MUT 4935 were isolated from *P. pavonica* and *P. oceanica*, respectively in the Mediterranean Sea (on average 3% salts). Interestingly, Jancic et al. (2015) detected β-glucosidase activity in six strains of *W. sebi* at concentration of NaCl up to 17%, that in this case might explain the ability to colonize these substrates.

4. Hypothetical ecological role

Although Ascomycota are dominant in the marine environment, the importance of Basidiomycota should not be neglected, considering the key role they play in the ecosystem and the large number of

potentially active metabolites produced in this unique habitat (Raghukumar, 2017). For instance, the degradation of recalcitrant molecules such as lignin and tannins by white rot fungi (e.g. *F. flavus*) increases the availability of cellulose or "ready to use" substances for other marine organisms. Hence, marine Basidiomycota are active in the cycle of nutrients and allow large quantities of biomass to return in the food chain of the ecosystem (Raghukumar, 2017).

The occurrence of these fungi in the sea is not accidental: most likely, they are metabolically active and live as saprobes, symbionts or parasites of plants and/or animals. It must be considered that in the sea, Basidiomycota rarely develop specialised reproductive structures (e.g. basidiomes), thus relegating their dispersion to hyphal fragments that would not freely survive in such a hostile environment unless they find a supporting substrate (biotic or abiotic). This indicates that marine Basidiomycota are not merely terrestrial contaminants; indeed, they may be the result of a selective pressure that has enabled them to live in unusual niches. Furthermore, marine Basidiomycota are often retrieved in their yeast form (Jones et al., 2015). This is not surprising, since yeasts are particularly adapted to aquatic environments (Libkind et al., 2017).

In 1972, Park classified aquatic micro-organisms as highly adapted "Indwellers", "Immigrants", whose main habitat is extra-aquatic or "Transients", that start to die and decrease their activities as soon as they reach a new environment and as a result, have no ecological significance. The Basidiomycota investigated in this work, were isolated on CMASW (3.4% Sea Salt) and the majority of them were not growing in the absence of salts, indicating the development of adaptation mechanisms.

In general, the ecological role of marine fungi is still largely unknown and, for the Basidiomycota here identified, we can only draw hypotheses based on evidences available in literature. For example, considering the anti-fungal properties of strains of *Coprinellus* sp. isolated from the Mediterranean sponge *Psammocinia* sp. (Paz et al. 2010) it can be speculated that the secretion of metabolites with antimicrobials in the marine environment may knock out other competitors and/or protect the host

from pathogens. Similar consideration can have the production of melanin (with antimicrobial and antitumor effects) by *S. commune*, a species commonly found in marine environments (Arun et al., 2015; Joel and Bhimba, 2013). Zhao et al. (2013), investigated a strain of *C. lacerata* recovered from the star fish *Acanthaster planci* and isolated compounds with antimicrobial activities (Ríos and Andújar, 2017).

Certainly, one could argue that spores of terrestrial fungi are washed into the Sea. However, the sporadic presence of an "Immigrant" fungus in the aquatic habitat, does not necessarily mean the it has no ecological significance (Park et al. 1972).

5. Conclusions

Basidiomycota are poorly represented in the marine environment and a definite estimate of the species inhabiting this ecosystem is still incomplete. This work demonstrates that i) many basidiomycetous fungi populate the coastal and oceanic marine ecosystems and that ii) accurate multi-locus molecular approaches are necessary for a correct taxonomic placement and identification. The last point is extremely important and could be a starting point for future studies aimed at shedding light on the ecological role of marine Basidiomycota, with a view to exploiting their great biotechnological potential.

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References

Appiah, T., Boakye, Y.D., Agyare, C., 2017. Antimicrobial Activities and Time-Kill Kinetics of Extracts of Selected Ghanaian Mushrooms. *Evidence-Based Complementary and Alternative Medicine* **15**.

Arun, G., Eyini, M., Gunasekaran, P., 2015. Characterization and biological activities of extracellular melanin produced by *Schizophyllum commune* (Fries). *Indian Journal of Experimental Biology* **53**: 380-387.

Binder, M., Justo, A., Riley, R., Salamov, A., Lopez-Giraldez, F., Sjokvist, E., Copeland, A., Foster, B., Sun, H., Larsson, E., Larsson, K.H., Townsend, J., Grigoriev, I.V., Hibbett, D.S., 2013. Phylogenetic and phylogenomic overview of the Polyporales. *Mycologia* **105**: 1350-1373.

Bodke, P.M., Senthilarasu, G., Raghukumar, S., 2012. Screening Diverse Fungi for Laccases of Varying Properties. *Indian Journal of Microbiology* **52**: 247-250.

Bonugli-Santos, R.C., Durrant, L.R., Sette, L.D., 2012. The Production of ligninolytic enzymes by marine-derived basidiomycetes and their biotechnological potential in the biodegradation of recalcitrant pollutants and the treatment of textile effluents. *Water Air and Soil Pollution* **223**: 2333-2345.

Bonugli-Santos, R.C., Vieira, G.A.L., Collins, C., Fernandes, T.C.C., Marin-Morales, M.A., Murray, P., Sette, L.D., 2016. Enhanced textile dye decolorization by marine-derived basidiomycete *Peniophora* sp CBMAI 1063 using integrated statistical design. *Environmental Science and Pollution Research* **23**: 8659-8668.

Bovio, E., Garzoli, L., Poli, A., Prigione, V., Firsova, D., McCormack, G.P., Varese, G.C., 2018. The culturable mycobiota associated with three Atlantic sponges, including two new species: *Thelebolus balaustiformis* and *T. spongiae*. *Fungal Systematic and Evolution* **1**: 141-167.

Bovio, E., Gnavi, G., Prigione, V., Spina, F., Denaro, R., Yakimov, M., Calogero, R., Crisafi, F., Varese, G.C., 2017. The culturable mycobiota of a Mediterranean marine site after an oil spill: isolation, identification and potential application in bioremediation. *Sci Total Environ* **576**: 310-318.

Brandao, L.R., Libkind, D., Vaz, A.B.M., Santo, L.C.E., Moline, M., de Garcia, V., van Broock, M., Rosa, C.A., 2011. Yeasts from an oligotrophic lake in Patagonia (Argentina): diversity, distribution and synthesis of photoprotective compounds and extracellular enzymes. Fems *Microbiology Ecology* **76**: 1-13.

Carlson, A., Justo, A., Hibbett, D.S., 2014. Species delimitation in *Trametes*: a comparison of ITS, RPB1, RPB2 and TEF1 gene phylogenies. *Mycologia* **106**: 735-745.

Chang, C.F., Lee, C.F., Lin, K.Y., Liu, S.-M., 2016. Diversity of yeasts associated with the sea surface microlayer and underlying water along the northern coast of Taiwan. *Research in microbiology* **167**: 35-45.

Chang, M.-H., Kim, H.J., Jahng, K.Y., Hong, S.C., 2008. The isolation and characterization of Pseudozyma sp. JCC 207, a novel producer of squalene. *Applied Microbiology and Biotechnology* **78**: 963.

Dalmaso, G.Z.L., Ferreira, D., Vermelho, A.B., 2015. Marine extremophiles: a source of hydrolases for biotechnological applications. *Marine Drugs* **13**: 1925-1965.

Darriba, D., Taboada, G.L., Doallo, R., Posada, D., 2012. jModelTest 2: more models, new heuristics and parallel computing. *Nature Methods* **9**: 772-772.

Frank, J.L., Coffan, R.A., Southworth, D., 2010. Aquatic gilled mushrooms: *Psathyrella* fruiting in the Rogue River in southern Oregon. *Mycologia* **102**: 93-107.

Gadanho, M., Almeida, J., Sampaio, J.P., 2003. Assessment of yeast diversity in a marine environment in the south of portugal by microsatellite-primed PCR. *Antonie Van Leeuwenhoek International Journal of General and Molecular Microbiology* **84**: 217-227.

Gao, Z., Li, B.L., Zheng, C.C., Wang, G.Y., 2008. Molecular detection of fungal communities in the Hawaiian marine sponges Suberites zeteki and Mycale armata. *Applied and Environmental Microbiology* **74**: 6091-6101.

Garzoli, L., Poli, A., Prigione, V., Gnavi, G., Varese, G.C., 2018. Peacock tail with a fungal cocktail: first assessment of mycobiota associated with the brown alga Padina pavonica.*Fungal Ecology* In press.

Garzoli, L., Gnavi, G., Tamma, F., Tosi, S., Varese, G.C., Picco, A.M., 2015. Sink or swim: Updated knowledge on marine fungi associated with wood substrates in the Mediterranean Sea and hints about their potential to remediate hydrocarbons. *Progress in Oceanography* **137**: 140-148.

Gnavi, G., Garzoli, L., Poli, A., Prigione, V., Burgaud, G., Varese, G.C., 2017. The culturable mycobiota of *Flabellia petiolata*: First survey of marine fungi associated to a Mediterranean green alga. *Plos One* **12** (4): e0175941.

González-Martínez, S., Soria, I., Ayala, N., Portillo-López, A., 2017. Culturable halotolerant fungal isolates from Southern California Gulf sediments. *Open Agriculture* **2**: 292-299.

Goossens, E., Wijnants, M., Packet, D., Lemiere, F., 2016. Enhanced separation and analysis procedure reveals production of tri-acylated mannosylerythritol lipids by *Pseudozyma aphidis*. *Journal of Industrial Microbiology & Biotechnology* **43**: 1537-1550.

Hagler, A.N., Mendonça-Hagler, L.C., 1981. Yeasts from marine and estuarine waters with different levels of pollution in the state of Rio de Janeiro, Brazil. *Applied and Environmental Microbiology* **41**: 173-178.

Hallenberg, N., Larsson, E., Mahlapuu, M., 1996. Phylogenetic studies in *Peniophora*. *Mycological Research* **100**: 179-187.

Hibbett, D., Bauer, R., Binder, M., Giachini, A., Hosaka, K., Justo, A., Larsson, E., Larsson, K.-H., Lawrey, J.D., Nagy, L., Nilsson, R., Weiss, M., Thorn, R., 2014. 14 Agaricomycetes. Springer.
Hibbett, D.S., 1996. Phylogenetic evidence for horizontal transmission of group I introns in the nuclear ribosomal DNA of mushroom-forming fungi. Molecular Biology and Evolution 13, 903-917.
Hibbett, D.S., Binder, M., Bischoff, J.F., Blackwell, M., Cannon, P.F., Eriksson, O.E., Huhndorf, S., James, T., Kirk, P.M., Lucking, R., Lumbsch, H.T., Lutzoni, F., Matheny, P.B., McLaughlin, D.J., Powell, M.J., Redhead, S., Schoch, C.L., Spatafora, J.W., Stalpers, J.A., Vilgalys, R., Aime, M.C.,

Aptroot, A., Bauer, R., Begerow, D., Benny, G.L., Castlebury, L.A., Crous, P.W., Dai, Y.C., Gams, W., Geiser, D.M., Griffith, G.W., Gueidan, C., Hawksworth, D.L., Hestmark, G., Hosaka, K., Humber, R.A., Hyde, K.D., Ironside, J.E., Koljalg, U., Kurtzman, C.P., Larsson, K.H., Lichtwardt, R., Longcore, J., Miadlikowska, J., Miller, A., Moncalvo, J.M., Mozley-Standridge, S., Oberwinkler, F., Parmasto, E., Reeb, V., Rogers, J.D., Roux, C., Ryvarden, L., Sampaio, J.P., Schussler, A., Sugiyama, J., Thorn, R.G., Tibell, L., Untereiner, W.A., Walker, C., Wang, Z., Weir, A., Weiss, M., White, M.M., Winka, K., Yao, Y.J., Zhang, N., 2007. A higher-level phylogenetic classification of the Fungi. *Mycological Research* **111**: 509-547.

Jancic, S., Nguyen, H.D.T., Frisvad, J.C., Zalar, P., Schroers, H.J., Seifert, K.A., Gunde-Cimerman, N., 2015. Taxonomic revision of the *Wallemia sebi* species complex. *Plos One* **10**.

Jia, Y., Du, J.J., Fang, H., Zhao, G.Y., Tian, X.J., 2013. Inhibition of freshwater algal species by co-culture with two fungi. M*aterials Science & Engineering C-Materials for Biological Applications* **33**: 2451-2454.

Joel, E.L., Bhimba, B.V., 2013. A secondary metabolite with antibacterial activity produced by mangrove foliar fungus *Schizophyllum commune. International Journal of Chemical, Environmental & Biological Scienes* **1**: 4.

Jones, E.B.G., Suetrong, S., Sakayaroj, J., Bahkali, A.H., Abdel-Wahab, M.A., Boekhout, T., Pang, K.L., 2015. Classification of marine Ascomycota, Basidiomycota, Blastocladiomycota and Chytridiomycota. *Fungal Diversity* **73**: 1-72.

Jones, E.G., Pang, K.-L., 2012. Marine fungi and fungal-like organisms. Walter de Gruyter.

Justo, A., Hibbett, D.S., 2011. Phylogenetic classification of *Trametes* (Basidiomycota, Polyporales) based on a five-marker dataset. *Taxon* **60**: 1567-1583.

Kachalkin, A.V., 2014. Yeasts of the White Sea intertidal zone and description of *Glaciozyma litorale* sp nov. *Antonie Van Leeuwenhoek International Journal of General and Molecular Microbiology* **105**: 1073-1083.

Knežević, A., Živković, L., Stajić, M., Vukojević, J., Milovanović, I., Spremo-Potparević, B., 2015. Antigenotoxic effect of *Trametes* spp. extracts against DNA damage on human peripheral white blood cells. T*he Scientific World Journal* doi:10.1155/2015/146378.

Kolenova, K., Vrsanska, M., Biely, P., 2005. Purification and characterization of two minor endo-beta-1,4-xylanases of *Schizophyllum commune*. *Enzyme and Microbial Technology* **36**: 903-910.

Kruse, J., Doehlemann, G., Kemen, E., Thines, M., 2017. Asexual and sexual morphs of Moesziomyces revisited. *Ima Fungus* **8**: 117-129.

Kurtzman, C.P., Robnett, C.J., 1998. Identification and phylogeny of ascomycetous yeasts from analysis of nuclear large subunit (26S) ribosomal DNA partial sequences. *Antonie Van Leeuwenhoek International Journal of General and Molecular Microbiology* **73**: 331-371.

Lee, H., Jang, Y., Choi, Y.S., Kim, M.J., Lee, J., Hong, J.H., Lee, Y.M., Kim, G.H., Kim, J.J., 2014. Biotechnological procedures to select white rot fungi for the degradation of PAHs. *Journal of Microbiological Methods* **97**, 56-62.

Libkind, D., Buzzini, P., Turchetti, B., Rosa, C.A., 2017. Yeasts in continental and seawater, Yeasts in Natural Ecosystems: Diversity. Springer, pp. 1-61.

Lindner, D.L., Banik, M.T., 2011. Intragenomic variation in the ITS rDNA region obscures phylogenetic relationships and inflates estimates of operational taxonomic units in genus *Laetiporus*. *Mycologia* **103**: 731-740.

Liu, C.H., Huang, X., Xie, T.N., Duan, N., Xue, Y.R., Zhao, T.X., Lever, M.A., Hinrichs, K.U., Inagaki, F., 2017. Exploration of cultivable fungal communities in deep coal-bearing sediments from similar to 1.3 to 2.5 km below the ocean floor. *Environmental Microbiology* **19**: 803-818.

Liu, X.Z., Wang, Q.M., Theelen, B., Groenewald, M., Bai, F.Y., Boekhout, T., 2015. Phylogeny of tremellomycetous yeasts and related dimorphic and filamentous basidiomycetes reconstructed from multiple gene sequence analyses. *Studies in Mycology* **81**: 1-26.

Luo, W., Vrijmoed, L.L.P., Jones, E.B.G., 2005. Screening of marine fungi for lignocellulose-degrading enzyme activities. *Botanica Marina* **48**, 379-386.

Masak, J., Cejkova, A., Schreiberova, O., Rezanka, T., 2014. *Pseudomonas* biofilms: possibilities of their control. *Fems Microbiology Ecology* **89**: 1-14.

Matheny, P.B., 2005. Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (Inocybe; Agaricales). *Molecular Phylogenetics and Evolution* **35**: 1-20.

Matheny, P.B., Wang, Z., Binder, M., Curtis, J.M., Lim, Y.W., Nilsson, R.H., Hughes, K.W., Hofstetter, V., Ammirati, J.F., Schoch, C.L., Langer, E., Langer, G., McLaughlin, D.J., Wilson, A.W., Froslev, T., Ge, Z.W., Kerrigan, R.W., Slot, J.C., Yang, Z.L., Baroni, T.J., Fischer, M., Hosaka, K., Matsuura, K., Seidl, M.T., Vauras, J., Hibbett, D.S., 2007. Contributions of rpb2 and tef1 to the phylogeny of mushrooms and allies (Basidiomycota, Fungi). *Molecular Phylogenetics and Evolution* **43**: 430-451.

Menezes, C.B.A., Bonugli-Santos, R.C., Miqueletto, P.B., Passarini, M.R.Z., Silva, C.H.D., Justo, M.R., Leal, R.R., Fantinatti-Garboggini, F., Oliveira, V.M., Berlinck, R.G.S., Sette, L.D., 2010. Microbial diversity associated with algae, ascidians and sponges from the north coast of Sao Paulo state, Brazil. *Microbiological Research* **165**: 466-482.

Miettinen, O., Spirin, V., Vlasak, J., Rivoire, B., Stenroos, S., Hibbett, D.S., 2016. Polypores and genus concepts in Phanerochaetaceae (Polyporales, Basidiomycota). *Mycokeys* **17** 1-46.

Mokhtarnejad, L., Arzanlou, M., Babai-Ahari, A., Di Mauro, S., Onofri, A., Buzzini, P., Turchetti, B., 2016. Characterization of basidiomycetous yeasts in hypersaline soils of the Urmia Lake National Park, Iran. *Extremophiles* **20**: 915-928.

Mtui, G., Nakamura, Y., 2008. Lignocellulosic enzymes from *Flavodon flavus*, a fungus isolated from Western Indian Ocean off the coast of Dar es Salaam, Tanzania. *African Journal of Biotechnology* **7**: 3066-3072.

Nagahama, T., Hamamoto, M., Nakase, T., Takami, H., Horikoshi, K., 2001. Distribution and identification of red yeasts in deep-sea environments around the northwest Pacific Ocean. *Antonie Van Leeuwenhoek International Journal of General and Molecular Microbiology* **80**: 101-110.

Nagy, L.G., Vagvolgyi, C., Papp, T., 2013. Morphological characterization of clades of the Psathyrellaceae (Agaricales) inferred from a multigene phylogeny. *Mycological Progress* **12**: 505-517.

Naim, M.A., Smidt, H., Sipkema, D., 2017. Fungi found in Mediterranean and North Sea sponges: how specific are they? *Peerj* **5**: 19.

Nguyen, H.D.T., Jancic, S., Meijer, M., Tanney, J.B., Zalar, P., Gunde-Cimerman, N., 2015. Application of the phylogenetic species concept to *Wallemia sebi* from house dust and indoor air revealed by multi-locus genealogical concordance, 2015). *Plos One* **10**: e0120894

Orgaz, B., Kives, J., Pedregosa, A.M., Monistrol, I.F., Laborda, F., SanJose, C., 2006. Bacterial biofilm removal using fungal enzymes. *Enzyme and Microbial Technology* **40**: 51-56.

Orstadius, L., Ryberg, M., Larsson, E., 2015. Molecular phylogenetics and taxonomy in Psathyrellaceae (Agaricales) with focus on psathyrelloid species: introduction of three new genera and 18 new species. *Mycological Progress* **14**: 42.

Paluselli, A., Aminot, Y., Galgani, F., Net, S., Sempéré, R., 2017. Occurrence of phthalate acid esters (PAEs) in the northwestern Mediterranean Sea and the Rhone River. *Progress in Oceanography* **160** doi.org/10.1016/j.pocean.2017.06.002

Panno, L., Bruno, M., Voyron, S., Anastasi, A., Gnavi, G., Miserere, L., Varese, G.C., 2013. Diversity, ecological role and potential biotechnological applications of marine fungi associated to the seagrass *Posidonia oceanica*. *New Biotechnology* **30**: 685-694.

Park D., 1972. On the ecology of heterotrophic micro-organisms in fresk-water. *Transaction of the British Mycological Society* **58**: 291-299.

Passarini, M.R.Z., Miqueletto, P.B., de Oliveira, V.M., Sette, L.D., 2015. Molecular diversity of fungal and bacterial communities in the marine sponge *Dragmacidon reticulatum*. J*ournal of Basic Microbiology* **55**: 207-220.

Paz, Z., Komon-Zelazowska, M., Druzhinina, I.S., Aveskamp, M.M., Shnaiderman, A., Aluma, Y., Carmeli, S., Ilan, M., Yarden, O., 2010. Diversity and potential antifungal properties of fungi associated with a Mediterranean sponge. *Fungal Diversity* **42**: 17-26.

Qin, X.Y., Yang, K.L., Li, J., Wang, C.Y., Shao, C.L., 2015. Phylogenetic diversity and antibacterial activity of culturable fungi derived from the zoanthid *Palythoa haddoni* in the South China Sea. *Marine Biotechnology* **17**: 99-109.

Raghukumar, C., D'Souza-Ticlo, D., Verma, A.K., 2008. Treatment of colored effluents with lignin-degrading enzymes: an emerging role of marine-derived fungi. *Crit Rev Microbiol* **34**: 189-206.

Raghukumar, S., 2017. Fungi in coastal and oceanic marine ecosystems: Marine fungi. Springer, Switzerland.

Raja, H.A., Miller, A.N., Pearce, C.J., Oberlies, N.H., 2017. Fungal Identification Using Molecular Tools: A Primer for the Natural Products Research Community. J*ournal of Natural Products* **80**: 756-770.

Richards, T.A., Jones, M.D., Leonard, G., Bass, D., 2012. Marine fungi: their ecology and molecular diversity. *Ann Rev Mar Sci* **4**: 495-522.

Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A., Hohna, S., Larget, B., Liu, L., Suchard, M.A., Huelsenbeck, J.P., 2012. MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. *Systematic Biology* **61**: 539-542.

Rytioja, J., Hildén, K., Yuzon, J., Hatakka, A., de Vries, R.P., Mäkelä, M.R., 2014. Plant-polysaccharide-degrading enzymes from Basidiomycetes. *Microbiol Mol Biol Rev* **78**: 614-649.

Ríos, J.-L., Andújar, I., 2017. Lanostanoids from Fungi as Potential Medicinal Agents. *Fungal Metabolites* 931-964.

Sabri, A., Bare, G., Jacques, P., Jabrane, A., Ongena, M., Van Heugen, J.C., Devreese, B., Thonart, P., 2001. Influence of moderate temperatures on myristoyl-CoA metabolism and acyl-CoA thioesterase activity in the psychrophilic antarctic yeast *Rhodotorula aurantiaca*. J*ournal of Biological Chemistry* **276**: 12691-12696.

Sakayaroj, J., Preedanon, S., Supaphon, O., Jones, E.B.G., Phongpaichit, S., 2010. Phylogenetic diversity of endophyte assemblages associated with the tropical seagrass *Enhalus acoroides* in Thailand. *Fungal Diversity* **42**: 27-45.

Siqueira, J.P.Z., Sutton, D., Gene, J., Garcia, D., Guevara-Suarez, M., Decock, C., Wiederhold, N., Guarro, J., 2016. *Schizophyllum radiatum,* an emerging fungus from human respiratory tract. *Journal of Clinical Microbiology* **54**: 2491-2497.

Song, X., Wang, X., Tan, Y., Feng, Y., Li, W., Cui, Q., 2015. High production of squalene using a newly isolated yeast-like strain Pseudozyma sp. SD301. *Journal of agricultural and food chemistry* **63**: 8445-8451.

Stamatakis, A., 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* **30**: 1312-1313.

Stielow, J., Lévesque, C., Seifert, K., Meyer, W., Iriny, L., Smits, D., Renfurm, R., Verkley, G., Groenewald, M., Chaduli, D., 2015. One fungus, which genes? Development and assessment of universal primers for potential secondary fungal DNA barcodes. *Persoonia: Molecular Phylogeny and Evolution of Fun*gi **35**: 242-263.

Tigini, V., Spina, F., Romagnolo, A., Prigione, V., Varese, G.C., 2013. Effective Biological Treatment of landfill leachates by means of selected white rot fungi. I*cheap-11: 11th International Conference on Chemical and Process Engineering*, Pts 1-4 32, 265-270.

Treu, R., Falandysz, J., 2017. Mycoremediation of hydrocarbons with basidiomycetes-a review. *Journal of Environmental Science and Health Part B-Pesticides Food Contaminants and Agricultural Wastes* **52**: 148-155.

Turchetti, B., Goretti, M., Branda, E., Diolaiuti, G., D'Agata, C., Smiraglia, C., Onofri, A., Buzzini, P., 2013. Influence of abiotic variables on culturable yeast diversity in two distinct Alpine glaciers. *Fems Microbiology Ecology* **86**: 327-340.

Vaidya, G., Lohman, D.J., Meier, R., 2011. SequenceMatrix: concatenation software for the fast assembly of multi-gene datasets with character set and codon information. *Cladistics* **27**: 171-180.

Vilgalys, R., Hester, M., 1990. Rapid genetic identification and mapping of enzymatically amplified ribosomal dna from several *Cryptococcus* species. *Journal of Bacteriology* **172**: 4238-4246.

Wang, J.W., Luo, Z.H., Xu, W., Ding, J.F., Zheng, T.L., 2016. Transformation of dimethyl phthalate esters (DMPEs) by a marine red yeast *Rhodotorula mucilaginosa* isolated from deep sea sediments of the Atlantic Ocean. *International Biodeterioration & Biodegradation* **109**: 223-228.

Wang, Q.M., Begerow, D., Groenewald, M., Liu, X.Z., Theelen, B., Bai, F.Y., Boekhout, T., 2015a. Multigene phylogeny and taxonomic revision of yeasts and related fungi in the Ustilaginomycotina. *Studies in Mycology* **81**: 55-83.

Wang, Q.M., Groenewald, M., Takashima, M., Theelen, B., Han, P.J., Liu, X.Z., Boekhout, T., Bai, F.Y., 2015b. Phylogeny of yeasts and related filamentous fungi within Pucciniomycotina determined from multigene sequence analyses. *Studies in Mycology* **81**: 27-53.

White, T.J., Bruns, T., Lee, S., Taylor, J., 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR protocols: a guide to methods and applications* **18**: 315-322.

Wuczkowski, M., Passoth, V., Turchetti, B., Andersson, A.C., Olstorpe, M., Laitila, A., Theelen, B., van Broock, M., Buzzini, P., Prillinger, H., Sterflinger, K., Schnurer, J., Boekhout, T., Libkind, D., 2011. Description of *Holtermanniella* gen. nov., including *Holtermanniella takashimae* sp. nov. and four new combinations, and proposal of the order Holtermanniales to accommodate

tremellomycetous yeasts of the Holtermannia clade. *International Journal of Systematic and Evolutionary Microbiology* **61**: 680-689.

Zalar, P., de Hoog, G.S., Schroers, H.J., Frank, J.M., Gunde-Cimerman, N., 2005. Taxonomy and phylogeny of the xerophilic genus *Wallemia* (Wallemiomycetes and Wallemiales, cl. et ord. nov.). *Antonie Van Leeuwenhoek International Journal of General and Molecular Microbiology* **87**: 311-328.

Zhang, L.K., Kang, M.Y., Huang, Y.C., Yang, L.X., 2016. Fungal communities from the calcareous deep-sea sediments in the Southwest India Ridge revealed by Illumina sequencing technology. *World Journal of Microbiology & Biotechnology* **32**: 11.

Zhang, T., Zaho, L., YU, C., Wei, T., Yu, L., 2017. Diversity and bioactivity of cultured aquatic fungi from the High Arctic region. *Advances in Polar Science* **28**: 29-42.

Zhao, Y., Li, S.Q., Li, H.J., Lan, W.J., 2013. Lanostane triterpenoids from the fungus *Ceriporia lacerata* associated with *Acanthaster planci*. *Chemistry of Natural Compounds* **49**: 653-656.

Zoz, L., Carvalho, J.C., Soccol, V.T., Casagrande, T.C., Cardoso, L., 2015. Torularhodin and Torulene: bioproduction, properties and prospective applications in food and cosmetics - a Review. *Brazilian Archives of Biology and Technology* **58**: 278-288.

CAPTIONS TO ILLUSTRATIONS

Figure 1. Bayesian phylogram of Psathyrellaceae (Agaricales) based on a combined nrITS, nrLSU and *ef-1α* dataset. The tree is rooted to *Agrocybe praecox*. Branch numbers indicate BPP values; Bar = expected changes per site (0.03).

Figure 2. Bayesian phylogram of Schizophyllaceae (Agaricales) based on a combined nrITS, nrLSU and *ef-1α* The tree is midpoint rooted. Branch numbers indicate BPP values; Bar = expected changes per site (0.007).

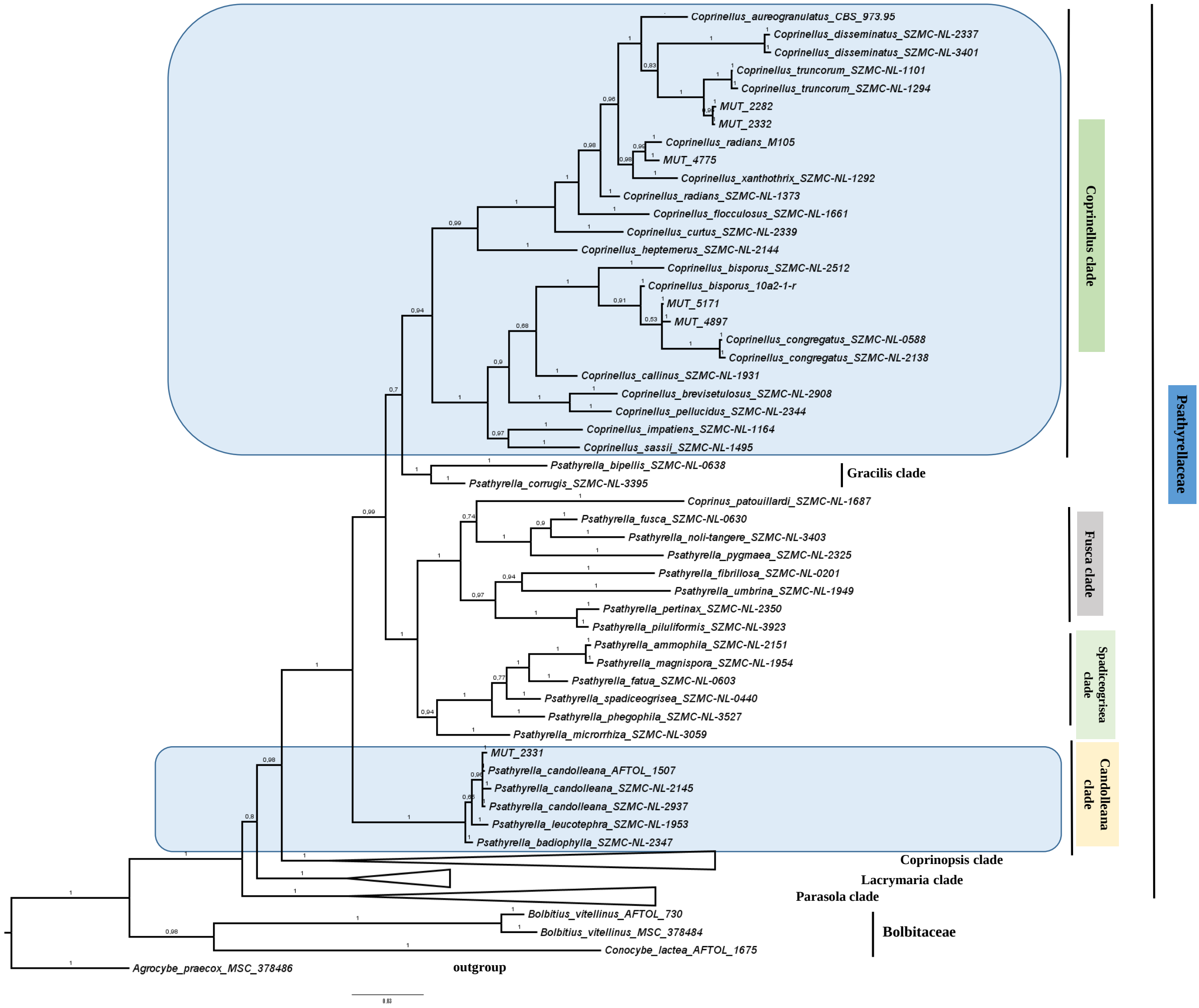
Figure 3. Bayesian phylogram of Peniophoraceae (Russulales) based on nrITS. The tree is rooted to the section *Validae* of Amanita, Agaricales (*Amanita rubescens* and *A. citrina*). Branch numbers indicate BPP values; Bar = expected changes per site (0.05).

Figure 4. Bayesian phylogram of the Phleboid clade of Polyporales based on a combined nrITS, nrLSU and *ef-1α* dataset. The tree is rooted to *Heterobasidion annosum*. Branch numbers indicate BPP values; Bar = expected changes per site (0.04).

Figure 5. Bayesian phylogram of the genus *Trametes* (Polyporaceae) based on a combined nrITS, nrLSU, *ef-1α*, *rpb1* and *rpb2* dataset. The tree is rooted to *Lopharia cinerascens*. Branch numbers indicate BPP values; Bar = expected changes per site (0.04).

Figure 6. Bayesian phylogram of Cystobasidiomycetes/Microboryomycetes based on a combined nrITS, nrSSU, D1/D2 and *ef-1α* dataset. The tree is rooted to Ustilagomycotina (*Microstroma phylloplanum*). Branch numbers indicate BPP values; Bar = expected changes per site (0.08).

Figure 7. Bayesian phylogram of Wallemiales based on a combined nrITS, *rpb1*, *rpb2* and *tsr1* dataset. The midpoint rooted. Branch numbers indicate BPP values; Bar = expected changes per site (0.004).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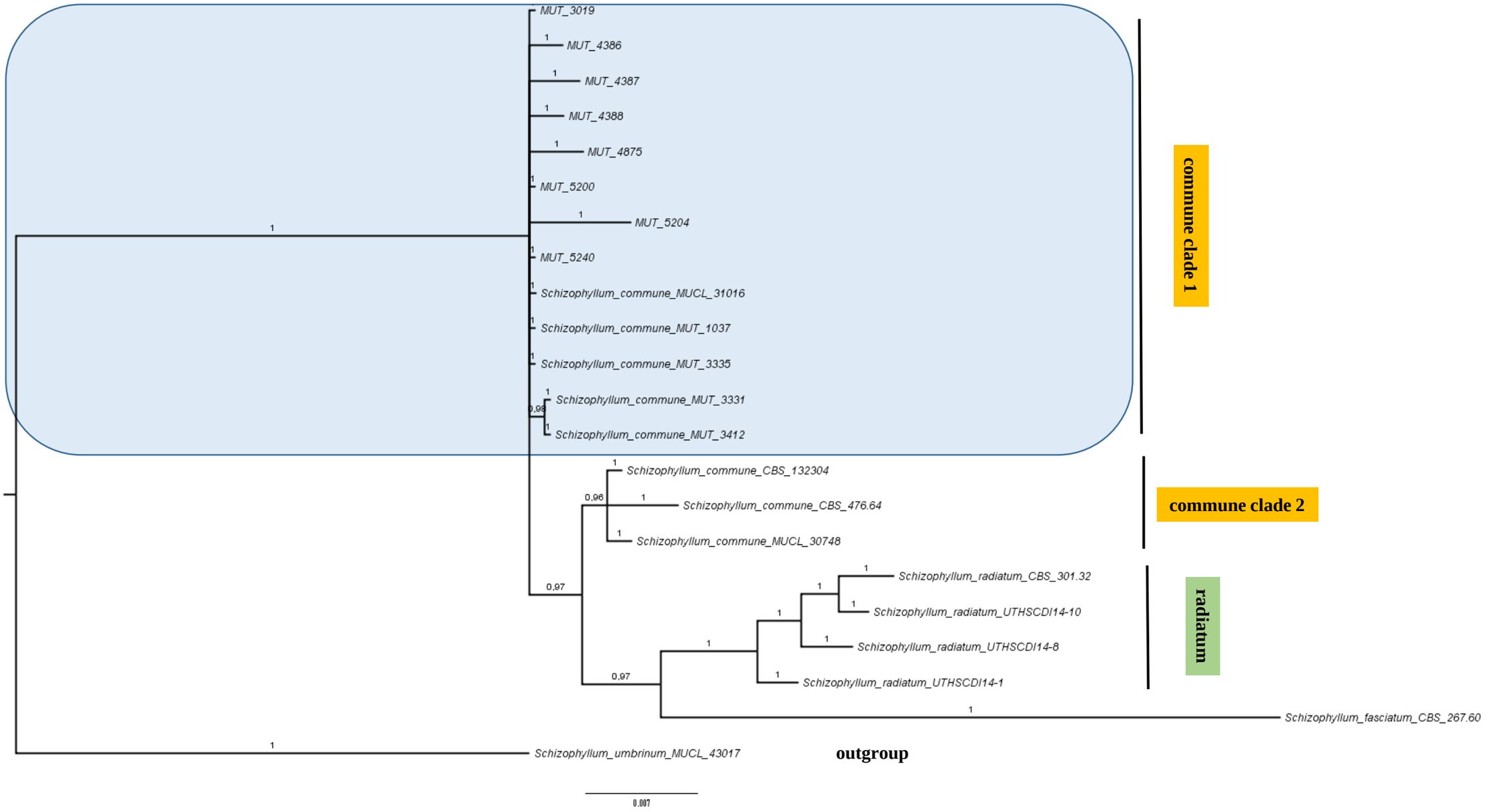
MUT_4897
Coprinellus_congregatus_SZMC-NL-0588
Coprinellus_congregatus_SZMC-NL-2138
Coprinellus_callinus_SZMC-NL-1931
Coprinellus_brevisetulosus_SZMC-NL-2908
Coprinellus_pellucidus_SZMC-NL-2344
Coprinellus_impatiens_SZMC-NL-1164
Coprinellus_sassii_SZMC-NL-1495
Psathyrella_bipellis_SZMC-NL-0638
Psathyrella_corrugis_SZMC-NL-3395
Coprinus_patouillardi_SZMC-NL-1687
Psathyrella_fusca_SZMC-NL-0630
Psathyrella_noli-tangere_SZMC-NL-3403
Psathyrella_pygmaea_SZMC-NL-2325
Psathyrella_fibrillosa_SZMC-NL-0201
Psathyrella_umbrina_SZMC-NL-1949
Psathyrella_pertinax_SZMC-NL-2350
Psathyrella_piluliformis_SZMC-NL-3923
Psathyrella_ammophila_SZMC-NL-2151
Psathyrella_magnispora_SZMC-NL-1954
Psathyrella_fatua_SZMC-NL-0603
Psathyrella_spadiceogrisea_SZMC-NL-0440
Psathyrella_phegophila_SZMC-NL-3527
Psathyrella_microrrhiza_SZMC-NL-3059
MUT_2331
Psathyrella_candolleana_AFTOL_1507
Psathyrella_candolleana_SZMC-NL-2145
Psathyrella_candolleana_SZMC-NL-2937
Psathyrella_leucotephra_SZMC-NL-1953
Psathyrella_badiophylla_SZMC-NL-2347
Bolbitius_vitellinus_AFTOL_730
Bolbitius_vitellinus_MSC_378484
Conocybe_lactea_AFTOL_1675
Agrocybe_praecox_MSC_378486
outgroup
Coprinellus clade
Gracilis clade
Fusca clade
Spadiceogrisea clade
Candolleana clade
Coprinopsis clade
Lacrymaria clade
Parasola clade
Bolbitaceae
Psathyrellaceae
0.03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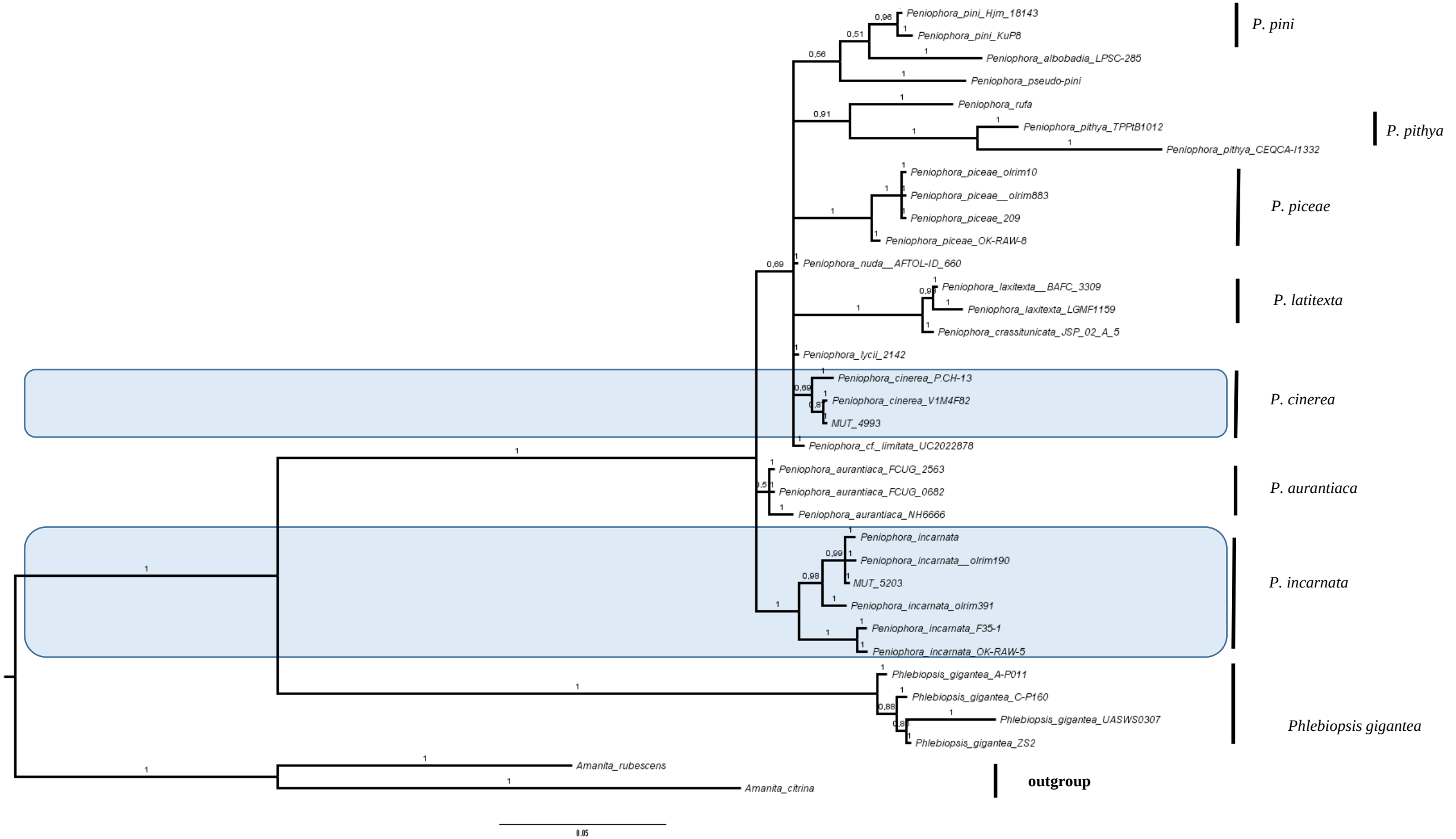
Schizophyllum_commune_MUT_1037
Schizophyllum_commune_MUT_3335
Schizophyllum_commune_MUT_3331
Schizophyllum_commune_MUT_3412
Schizophyllum_commune_CBS_132304
Schizophyllum_commune_CBS_476.64
Schizophyllum_commune_MUCL_30748
Schizophyllum_radiatum_CBS_301.32
Schizophyllum_radiatum_UTHSCDI14-10
Schizophyllum_radiatum_UTHSCDI14-8
Schizophyllum_radiatum_UTHSCDI14-1
Schizophyllum_fasciatum_CBS_267.60
Schizophyllum_umbrinum_MUCL_43017
commune clade 1
commune clade 2
radiatum
outgroup
0.007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Peniophora_pini_KuP8
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Peniophora_pseudo-pini
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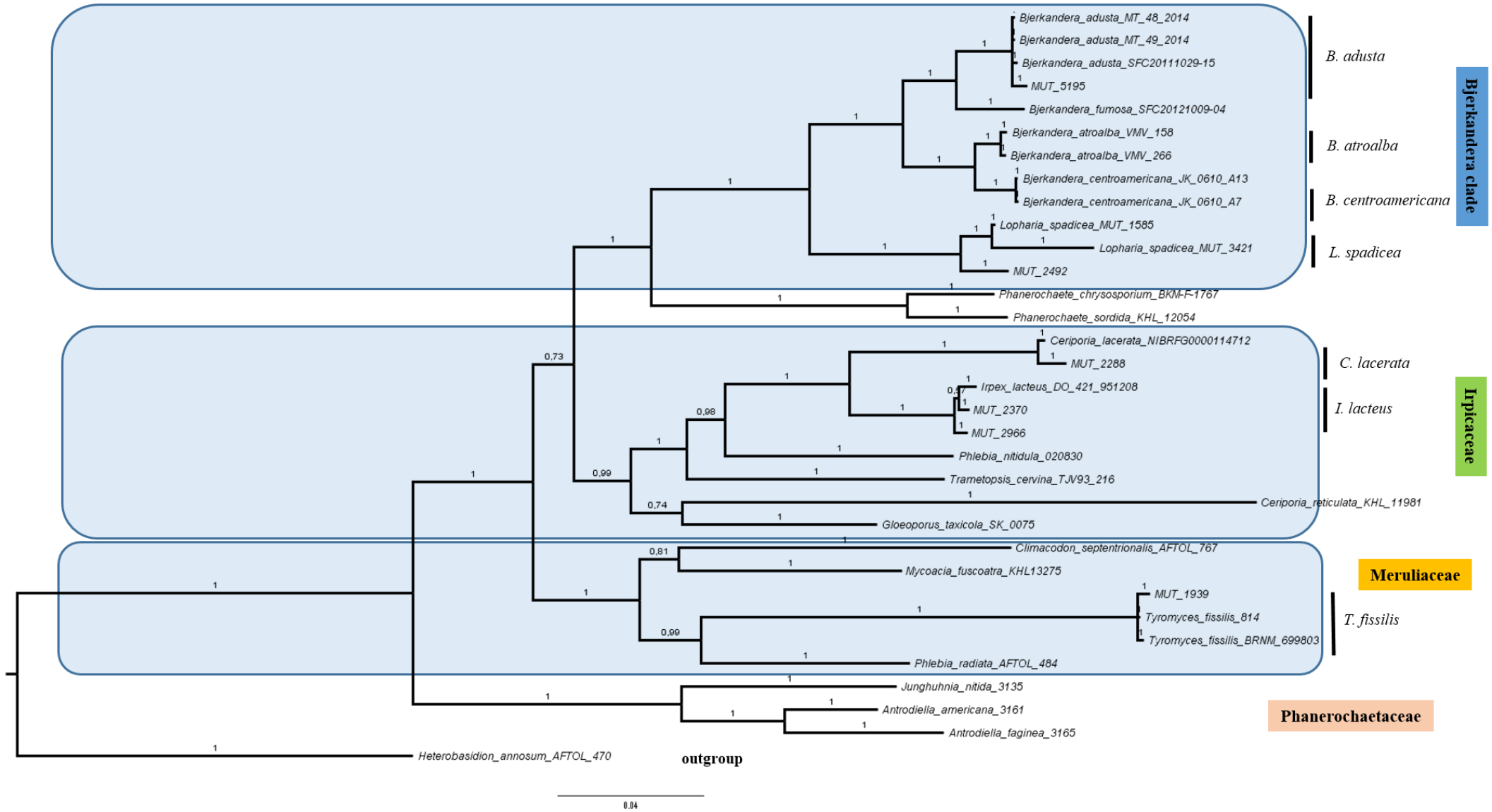
Peniophora_pithya_TPPtB1012
Peniophora_pithya_CEQCA-I1332
Peniophora_piceae_olrim10
Peniophora_piceae__olrim883
Peniophora_piceae_209
Peniophora_piceae_OK-RAW-8
Peniophora_nuda__AFTOL-ID_660
Peniophora_laxitexta__BAFC_3309
Peniophora_laxitexta_LGMF1159
Peniophora_crassitunicata_JSP_02_A_5
Peniophora_lycii_2142
Peniophora_cinerea_P.CH-13
Peniophora_cinerea_V1M4F82
MUT_4993
Peniophora_cf._limitata_UC2022878
Peniophora_aurantiaca_FCUG_2563
Peniophora_aurantiaca_FCUG_0682
Peniophora_aurantiaca_NH6666
Peniophora_incarnata
Peniophora_incarnata__olrim190
MUT_5203
Peniophora_incarnata_olrim391
Peniophora_incarnata_F35-1
Peniophora_incarnata_OK-RAW-5
Phlebiopsis_gigantea_A-P011
Phlebiopsis_gigantea_C-P160
Phlebiopsis_gigantea_UASWS0307
Phlebiopsis_gigantea_ZS2
Amanita_rubescens
Amanita_citrina
P. pini
P. pithya
P. piceae
P. latitexta
P. cinerea
P. aurantiaca
P. incarnata
Phlebiopsis gigantea
outgroup
0.05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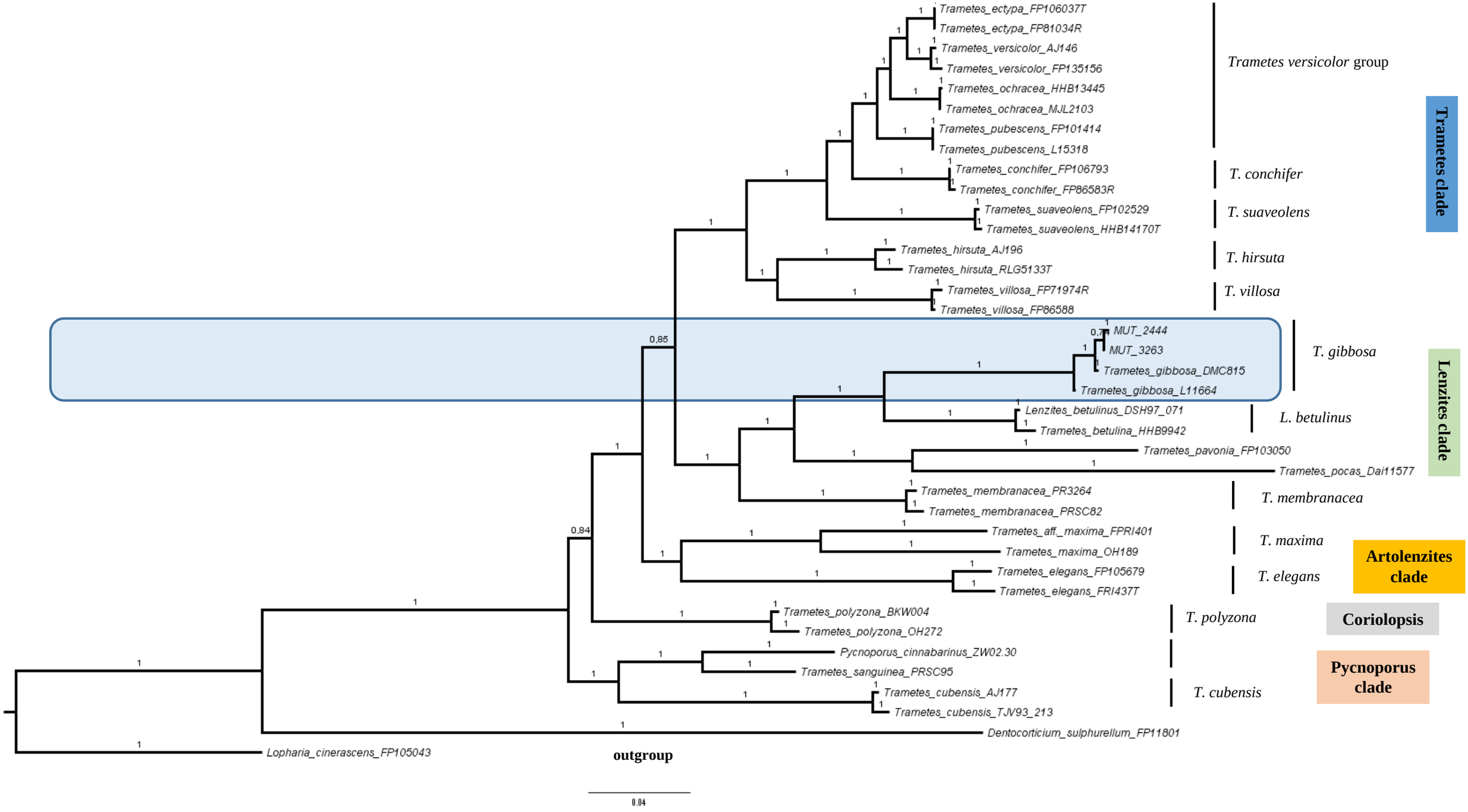
MUT_5195
Bjerkandera_fumosa_SFC20121009-04
Bjerkandera_atroalba_VMV_158
Bjerkandera_atroalba_VMV_266
Bjerkandera_centroamericana_JK_0610_A13
Bjerkandera_centroamericana_JK_0610_A7
Lopharia_spadicea_MUT_1585
Lopharia_spadicea_MUT_3421
MUT_2492
Phanerochaete_chrysosporium_BKM-F-1767
Phanerochaete_sordida_KHL_12054
Ceriporia_lacerata_NIBRFG0000114712
MUT_2288
Irpex_lacteus_DO_421_951208
MUT_2370
MUT_2966
Phlebia_nitidula_020830
Trametopsis_cervina_TJV93_216
Ceriporia_reticulata_KHL_11981
Gloeoporus_taxicola_SK_0075
Climacodon_septentrionalis_AFTOL_767
Mycoacia_fuscoatra_KHL13275
MUT_1939
Tyromyces_fissilis_814
Tyromyces_fissilis_BRNM_699803
Phlebia_radiata_AFTOL_484
Junghuhnia_nitida_3135
Antrodiella_americana_3161
Antrodiella_faginea_3165
Heterobasidion_annosum_AFTOL_470
outgroup
0.04
B. adusta
B. atroalba
B. centroamericana
L. spadicea
Bjerkandera clade
C. lacerata
I. lacteus
Irpicaceae
Meruliaceae
T. fissilis
Phanerochaetaceae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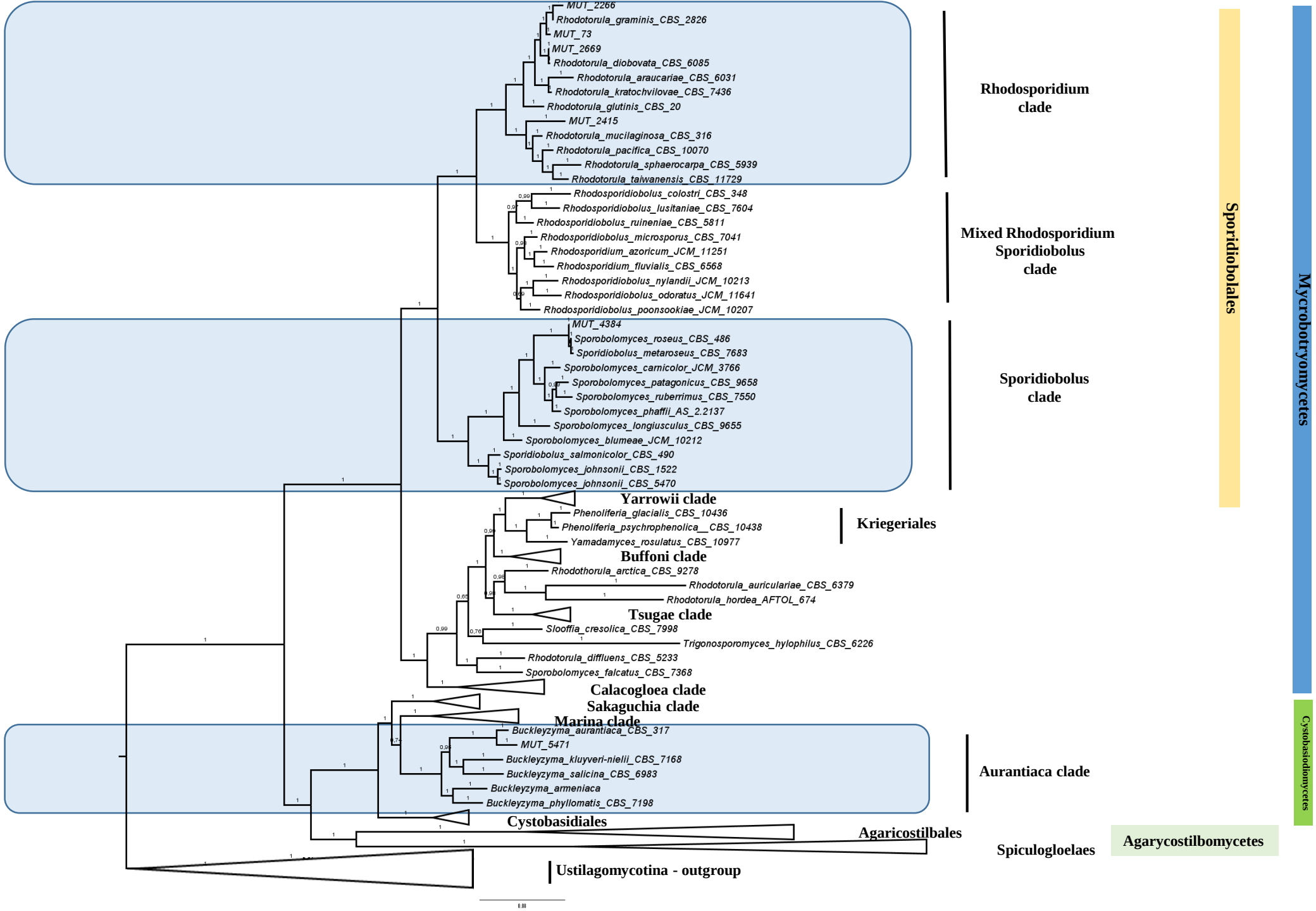
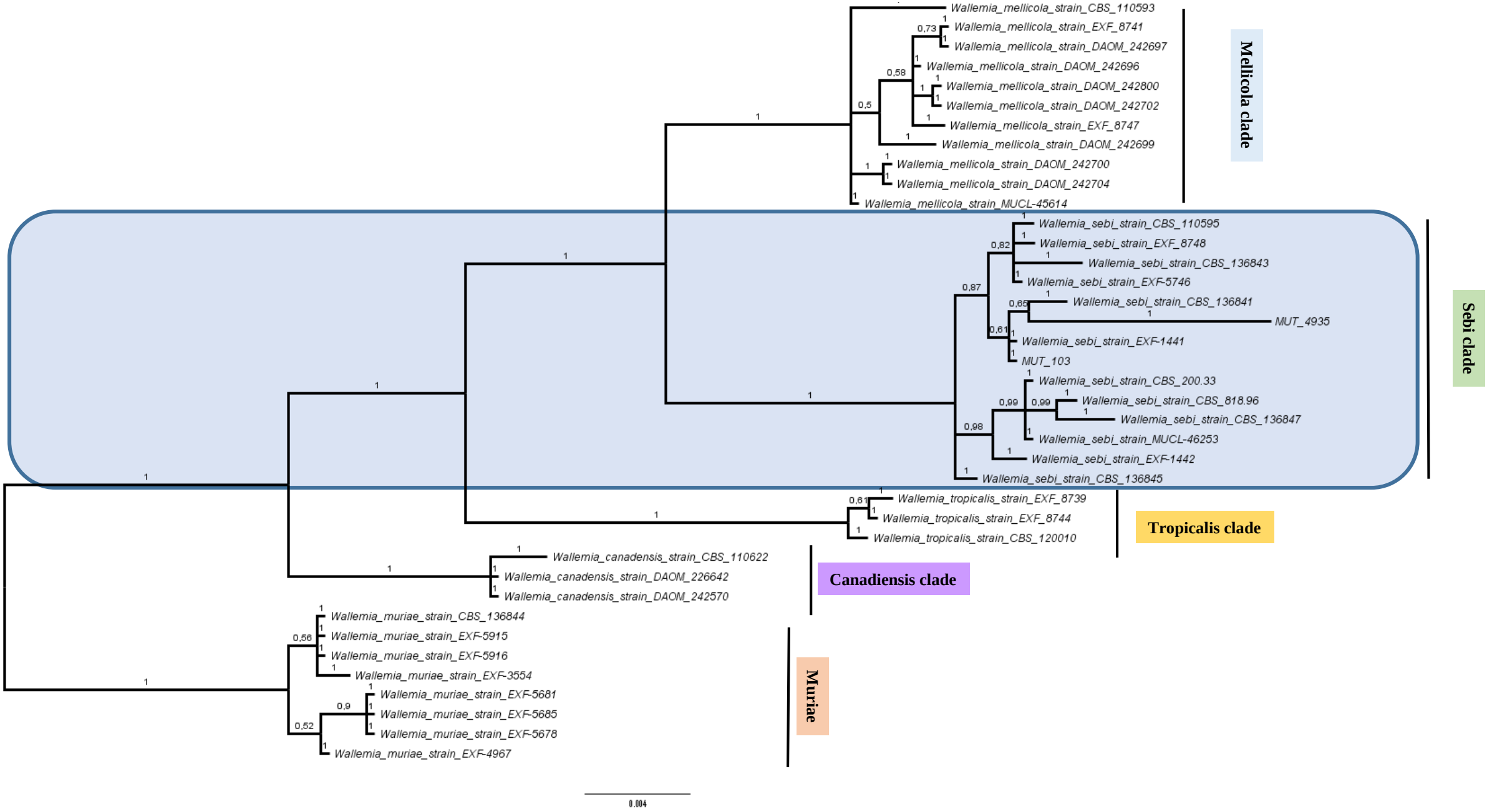
Trametes_ectypa_FP81034R
Trametes_versicolor_AJ146
Trametes_versicolor_FP135156
Trametes_ochracea_HHB13445
Trametes_ochracea_MJL2103
Trametes_pubescens_FP101414
Trametes_pubescens_L15318
Trametes versicolor group
Trametes_conchifer_FP106793
Trametes_conchifer_FP86583R
T. conchifer
Trametes_suaveolens_FP102529
Trametes_suaveolens_HHB14170T
T. suaveolens
Trametes_hirsuta_AJ196
Trametes_hirsuta_RLG5133T
T. hirsuta
Trametes_villosa_FP71974R
Trametes_villosa_FP86588
T. villosa
Trametes clade
MUT_2444
MUT_3263
Trametes_gibbosa_DMC815
Trametes_gibbosa_L11664
T. gibbosa
Lenzites_betulinus_DSH97_071
Trametes_betulina_HHB9942
L. betulinus
Trametes_pavonia_FP103050
Trametes_pocas_Dai11577
Lenzites clade
Trametes_membranacea_PR3264
Trametes_membranacea_PRSC82
T. membranacea
Trametes_aff._maxima_FPRI401
Trametes_maxima_OH189
T. maxima
Trametes_elegans_FP105679
Trametes_elegans_FRI437T
T. elegans
Artolenzites clade
Trametes_polyzona_BKW004
Trametes_polyzona_OH272
T. polyzona
Coriolopsis
Pycnoporus_cinnabarinus_ZW02.30
Trametes_sanguinea_PRSC95
Trametes_cubensis_AJ177
Trametes_cubensis_TJV93_213
T. cubensis
Pycnoporus clade
Dentocorticium_sulphurellum_FP11801
Lopharia_cinerascens_FP105043
outgroup
0,85
0,84
0.04


MUT_2266
Rhodotorula_graminis_CBS_2826
MUT_73
MUT_2669
Rhodotorula_diobovata_CBS_6085
Rhodotorula_araucariae_CBS_6031
Rhodotorula_kratochvilovae_CBS_7436
Rhodotorula_glutinis_CBS_20
MUT_2415
Rhodotorula_mucilaginosa_CBS_316
Rhodotorula_pacifica_CBS_10070
Rhodotorula_sphaerocarpa_CBS_5939
Rhodotorula_taiwanensis_CBS_11729
Rhodosporidiobolus_colostri_CBS_348
Rhodosporidiobolus_lusitaniae_CBS_7604
Rhodosporidiobolus_ruineniae_CBS_5811
Rhodosporidiobolus_microsporus_CBS_7041
Rhodosporidium_azoricum_JCM_11251
Rhodosporidium_fluvialis_CBS_6568
Rhodosporidiobolus_nylandii_JCM_10213
Rhodosporidiobolus_odoratus_JCM_11641
Rhodosporidiobolus_poonsookiae_JCM_10207
MUT_4384
Sporobolomyces_roseus_CBS_486
Sporidiobolus_metaroseus_CBS_7683
Sporobolomyces_carnicolor_JCM_3766
Sporobolomyces_patagonicus_CBS_9658
Sporobolomyces_ruberrimus_CBS_7550
Sporobolomyces_phaffii_AS_2.2137
Sporobolomyces_longiusculus_CBS_9655
Sporobolomyces_blumeae_JCM_10212
Sporidiobolus_salmonicolor_CBS_490
Sporobolomyces_johnsonii_CBS_1522
Sporobolomyces_johnsonii_CBS_5470
Yarrowii clade
Phenoliferia_glacialis_CBS_10436
Phenoliferia_psychrophenolica__CBS_10438
Yamadamyces_rosulatus_CBS_10977
Buffoni clade
Rhodothorula_arctica_CBS_9278
Rhodotorula_auriculariae_CBS_6379
Rhodotorula_hordea_AFTOL_674
Tsugae clade
Slooffia_cresolica_CBS_7998
Trigonosporomyces_hylophilus_CBS_6226
Rhodotorula_diffluens_CBS_5233
Sporobolomyces_falcatus_CBS_7368
Calacogloea clade
Sakaguchia clade
Marina clade
Buckleyzyma_aurantiaca_CBS_317
MUT_5471
Buckleyzyma_kluyveri-nielii_CBS_7168
Buckleyzyma_salicina_CBS_6983
Buckleyzyma_armeniaca
Buckleyzyma_phyllomatis_CBS_7198
Cystobasidiales
Agaricostilbales
Spiculogloelaes
Ustilagomycotina - outgroup
Rhodosporidium clade
Mixed Rhodosporidium Sporidiobolus clade
Sporidiobolus clade
Kriegeriales
Aurantiaca clade
Sporidiobolales
Mycrobotryomycetes
Cystobasiodiomycetes
Agarycostilbomycetes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Wallemia_mellicola_strain_EXF_8741
Wallemia_mellicola_strain_DAOM_242697
Wallemia_mellicola_strain_DAOM_242696
Wallemia_mellicola_strain_DAOM_242800
Wallemia_mellicola_strain_DAOM_242702
Wallemia_mellicola_strain_EXF_8747
Wallemia_mellicola_strain_DAOM_242699
Wallemia_mellicola_strain_DAOM_242700
Wallemia_mellicola_strain_DAOM_242704
Wallemia_mellicola_strain_MUCL-45614
Mellicola clade
Wallemia_sebi_strain_CBS_110595
Wallemia_sebi_strain_EXF_8748
Wallemia_sebi_strain_CBS_136843
Wallemia_sebi_strain_EXF-5746
Wallemia_sebi_strain_CBS_136841
MUT_4935
Wallemia_sebi_strain_EXF-1441
MUT_103
Wallemia_sebi_strain_CBS_200.33
Wallemia_sebi_strain_CBS_818.96
Wallemia_sebi_strain_CBS_136847
Wallemia_sebi_strain_MUCL-46253
Wallemia_sebi_strain_EXF-1442
Wallemia_sebi_strain_CBS_136845
Sebi clade
Wallemia_tropicalis_strain_EXF_8739
Wallemia_tropicalis_strain_EXF_8744
Wallemia_tropicalis_strain_CBS_120010
Tropicalis clade
Wallemia_canadensis_strain_CBS_110622
Wallemia_canadensis_strain_DAOM_226642
Wallemia_canadensis_strain_DAOM_242570
Canadiensis clade
Wallemia_muriae_strain_CBS_136844
Wallemia_muriae_strain_EXF-5915
Wallemia_muriae_strain_EXF-5916
Wallemia_muriae_strain_EXF-3554
Wallemia_muriae_strain_EXF-5681
Wallemia_muriae_strain_EXF-5685
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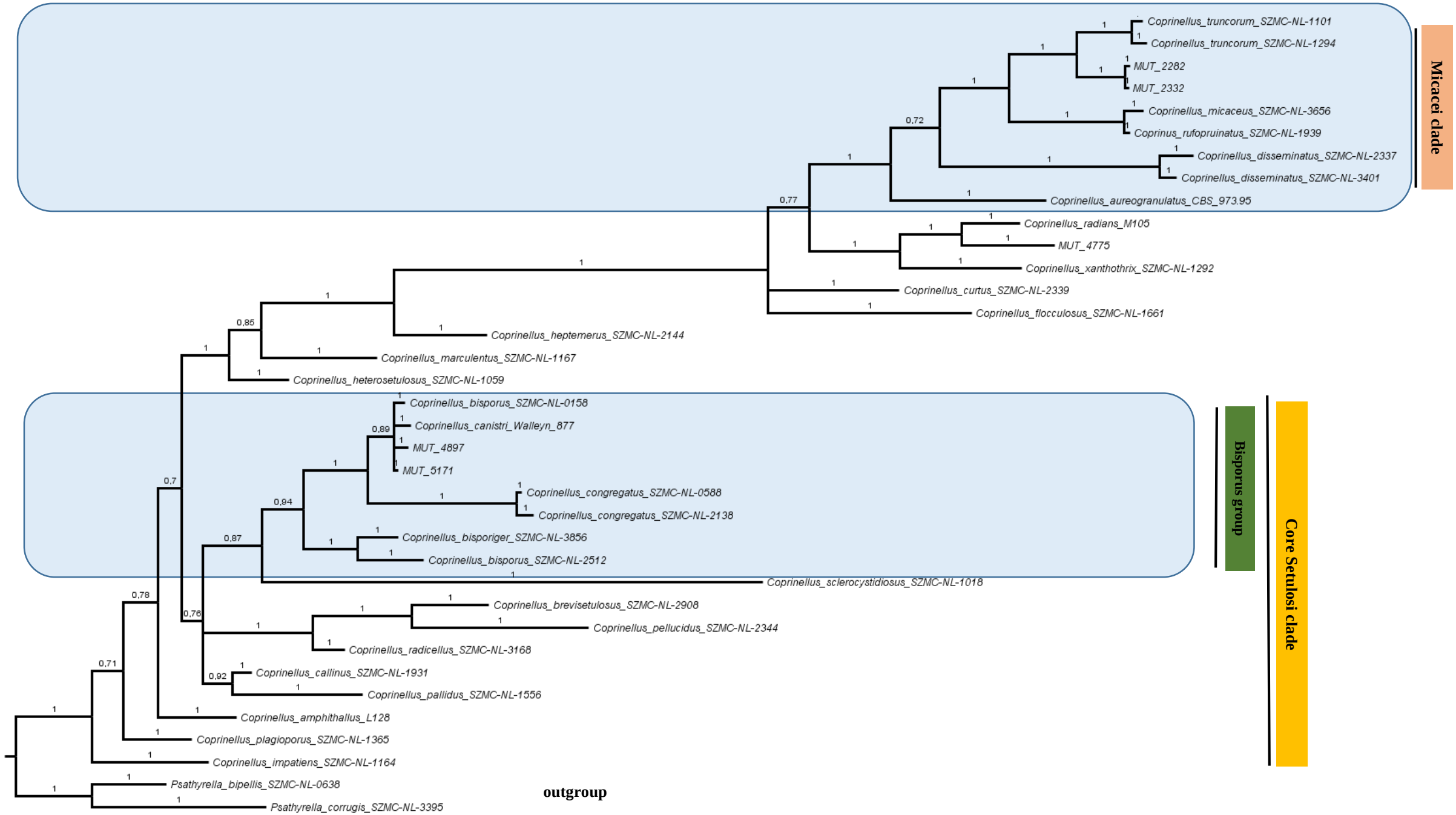
Wallemia_muriae_strain_EXF-4967
Muriae
0.004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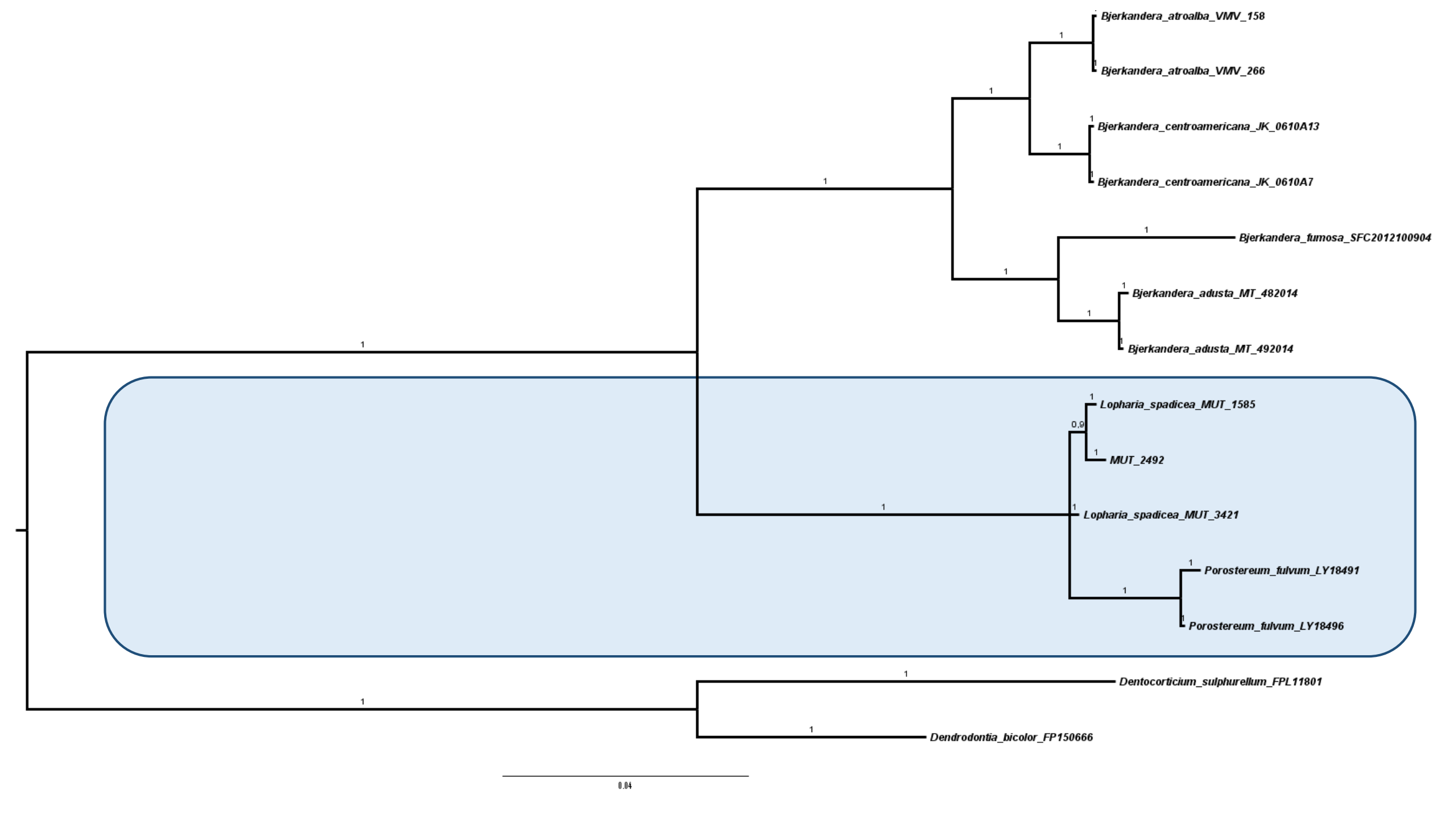
MUT_2282
MUT_2332
Coprinellus_micaceus_SZMC-NL-3656
Coprinus_rufopruinatus_SZMC-NL-1939
Coprinellus_disseminatus_SZMC-NL-2337
Coprinellus_disseminatus_SZMC-NL-3401
Coprinellus_aureogranulatus_CBS_973.95
Micacei clade
Coprinellus_radians_M105
MUT_4775
Coprinellus_xanthothrix_SZMC-NL-1292
Coprinellus_curtus_SZMC-NL-2339
Coprinellus_flocculosus_SZMC-NL-1661
Coprinellus_heptemerus_SZMC-NL-2144
Coprinellus_marculentus_SZMC-NL-1167
Coprinellus_heterosetulosus_SZMC-NL-1059
Coprinellus_bisporus_SZMC-NL-0158
Coprinellus_canistri_Walleyn_877
MUT_4897
MUT_5171
Coprinellus_congregatus_SZMC-NL-0588
Coprinellus_congregatus_SZMC-NL-2138
Coprinellus_bisporiger_SZMC-NL-3856
Coprinellus_bisporus_SZMC-NL-2512
Bisporus group
Coprinellus_sclerocystidiosus_SZMC-NL-1018
Coprinellus_brevisetulosus_SZMC-NL-2908
Coprinellus_pellucidus_SZMC-NL-2344
Coprinellus_radicellus_SZMC-NL-3168
Coprinellus_callinus_SZMC-NL-1931
Coprinellus_pallidus_SZMC-NL-1556
Coprinellus_amphithallus_L128
Coprinellus_plagioporus_SZMC-NL-1365
Coprinellus_impatiens_SZMC-NL-1164
Core Setulosi clade
Psathyrella_bipellis_SZMC-NL-0638
Psathyrella_corrugis_SZMC-NL-3395
outgroup
0.02


Bjerkandera_atroalba_VMV_158
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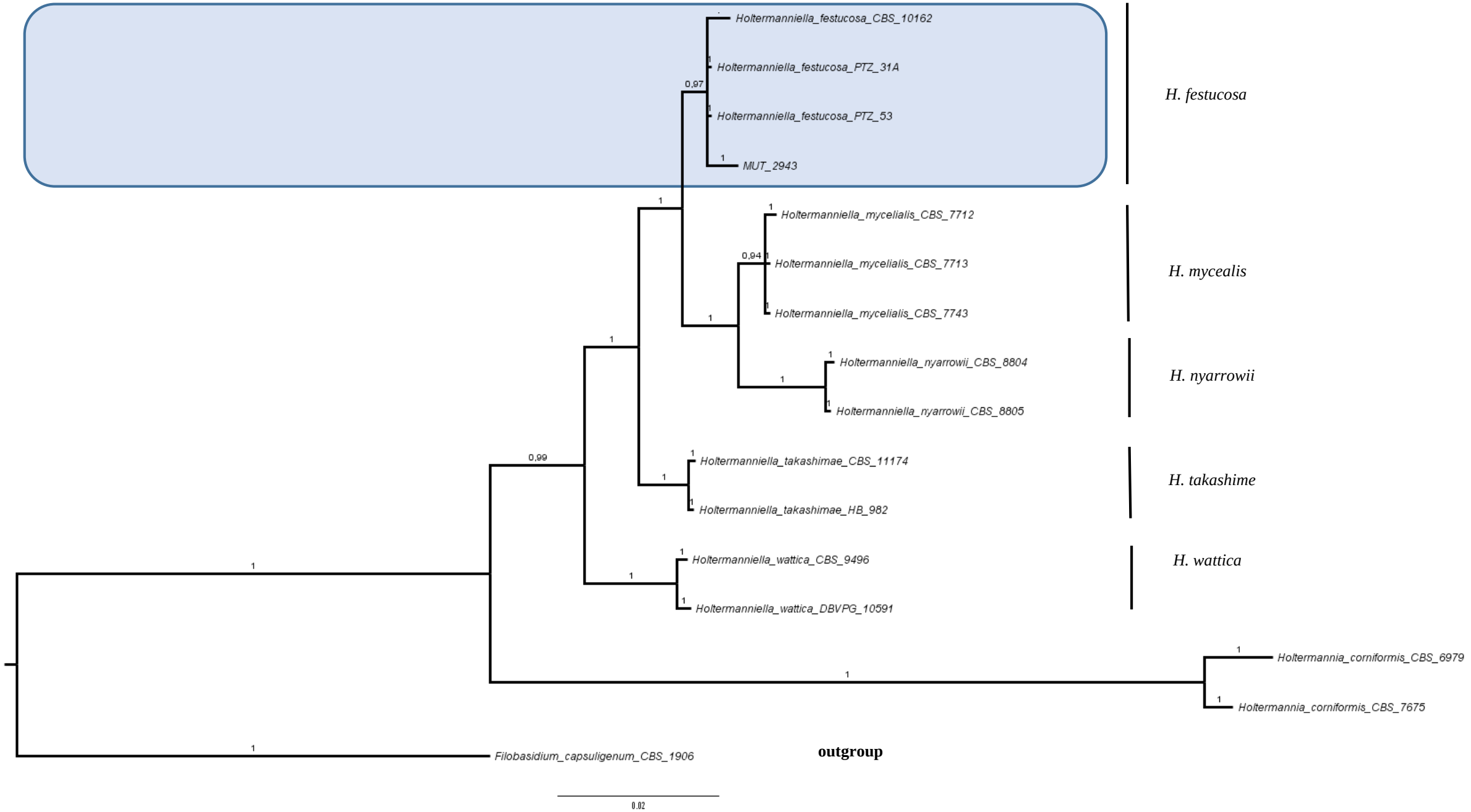
Bjerkandera_centroamericana_JK_0610A13
Bjerkandera_centroamericana_JK_0610A7
Bjerkandera_fumosa_SFC2012100904
Bjerkandera_adusta_MT_482014
Bjerkandera_adusta_MT_492014
Lopharia_spadicea_MUT_1585
MUT_2492
Lopharia_spadicea_MUT_3421
Porostereum_fulvum_LY18491
Porostereum_fulvum_LY18496
Dentocorticium_sulphurellum_FPL11801
Dendrodontia_bicolor_FP150666
0,9
0.04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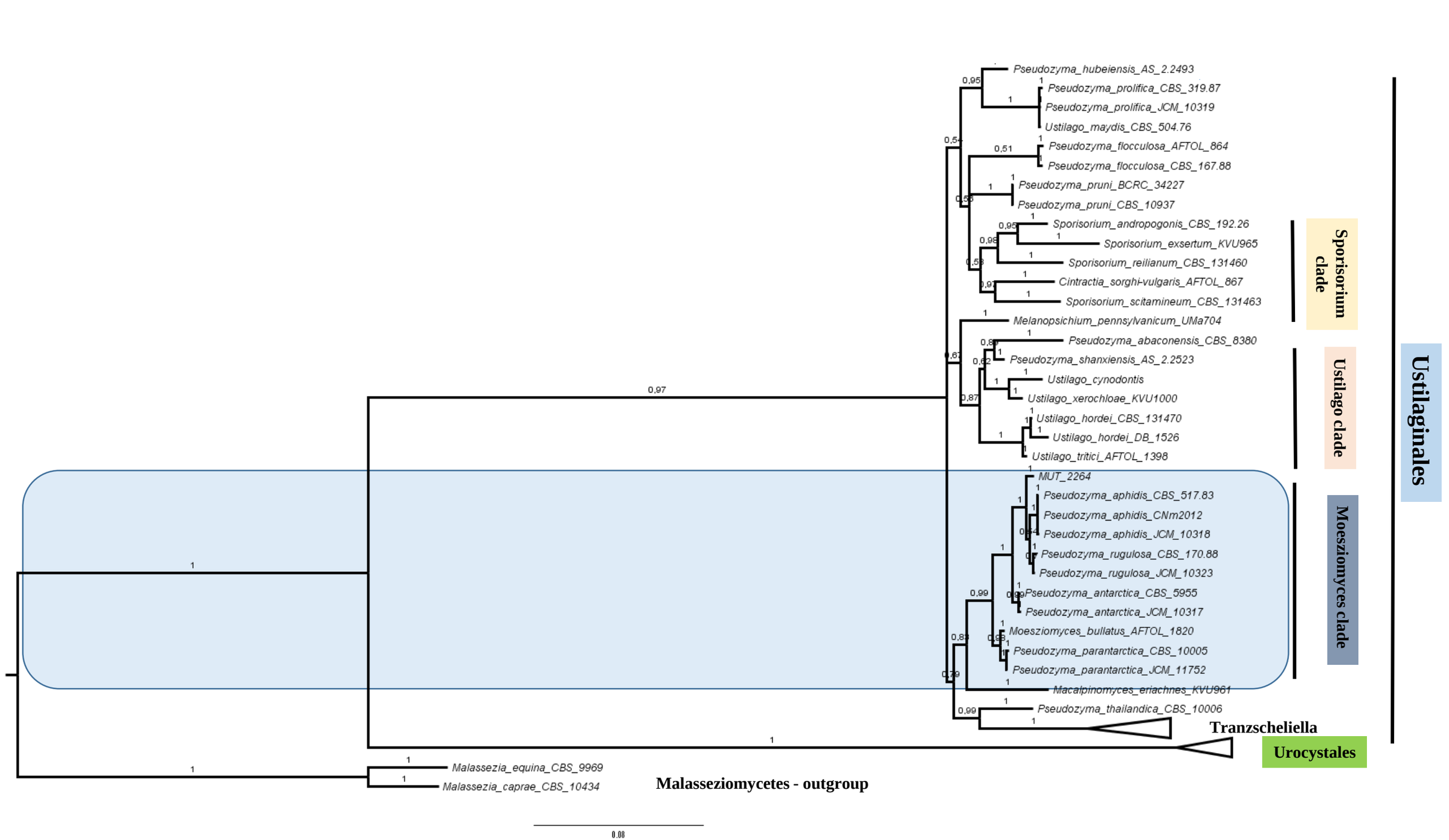
Holtermanniella_festucosa_PTZ_31A
Holtermanniella_festucosa_PTZ_53
MUT_2943
H. festucosa
Holtermanniella_mycelialis_CBS_7712
Holtermanniella_mycelialis_CBS_7713
Holtermanniella_mycelialis_CBS_7743
H. mycealis
Holtermanniella_nyarrowii_CBS_8804
Holtermanniella_nyarrowii_CBS_8805
H. nyarrowii
Holtermanniella_takashimae_CBS_11174
Holtermanniella_takashimae_HB_982
H. takashime
Holtermanniella_wattica_CBS_9496
Holtermanniella_wattica_DBVPG_10591
H. wattica
Holtermannia_corniformis_CBS_6979
Holtermannia_corniformis_CBS_7675
Filobasidium_capsuligenum_CBS_1906
outgroup
0,97
0,94
0,99
1
0.02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Pseudozyma_prolifica_CBS_319.87
Pseudozyma_prolifica_JCM_10319
Ustilago_maydis_CBS_504.76
Pseudozyma_flocculosa_AFTOL_864
Pseudozyma_flocculosa_CBS_167.88
Pseudozyma_pruni_BCRC_34227
Pseudozyma_pruni_CBS_10937
Sporisorium_andropogonis_CBS_192.26
Sporisorium_exsertum_KVU965
Sporisorium_reilianum_CBS_131460
Cintractia_sorghi-vulgaris_AFTOL_867
Sporisorium_scitamineum_CBS_131463
Melanopsichium_pennsylvanicum_UMa704
Pseudozyma_abaconensis_CBS_8380
Pseudozyma_shanxiensis_AS_2.2523
Ustilago_cynodontis
Ustilago_xerochloae_KVU1000
Ustilago_hordei_CBS_131470
Ustilago_hordei_DB_1526
Ustilago_tritici_AFTOL_1398
MUT_2264
Pseudozyma_aphidis_CBS_517.83
Pseudozyma_aphidis_CNm2012
Pseudozyma_aphidis_JCM_10318
Pseudozyma_rugulosa_CBS_170.88
Pseudozyma_rugulosa_JCM_10323
Pseudozyma_antarctica_CBS_5955
Pseudozyma_antarctica_JCM_10317
Moesziomyces_bullatus_AFTOL_1820
Pseudozyma_parantarctica_CBS_10005
Pseudozyma_parantarctica_JCM_11752
Macalpinomyces_eriachnes_KVU961
Pseudozyma_thailandica_CBS_10006
Tranzscheliella
Urocystales
Malassezia_equina_CBS_9969
Malassezia_caprae_CBS_10434
Malasseziomycetes - outgroup
0.08
Sporisorium clade
Ustilago clade
Moesziomyces clade
Ustilaginales

Table 1. List of strains analysed. Source of isolation, final identification and GenBank accession numbers relative to the markers amplified and sequenced.

STRAIN	SUBSTRATE	IDENTIFICATION	*nrITS*	*nrLSU*	*nrSSU*	*D1/D2 (nrLSU)*	*ef-1α*	*rpb1*	*rpb2*	*tsr1*
Agaricomyectes										
Agaricales										
Psathyrellaceae										
MUT 2331	*Grantia compressa*	***Psathyrella candolleana***	MF125293	MF125290	--	--	--	--	--	--
MUT 2332	*Grantia compressa*	***Coprinellus sp.***	MF140469	MF140461	--	--	--	MF282006	--	--
MUT 2282	*Grantia compressa*	***Coprinellus sp.***	MF140467	MF140459	--	--	MF150864	MF282004	--	--
MUT 4775	*Flabellia petiolata*	***Coprinellus radians***	KR014370§	KP671736§	--	--	MF150868	--	--	--
MUT 4897	*Padina pavonica*	***Coprinellus sp.***	KM355983	MF140457	KM355995	--	MF150860	MF282001	--	--
MUT 5171	*Padina pavonica*	***Coprinellus sp.***	KT699134	MF140458	--	--	MF150861	MF282002	--	--
Schizophyllaceae										
MUT 3019	*Aplysina cavernicola*	***Schizophyllum commune***	MF098694	MF115836	--	--	MF136466	--	--	--
MUT 4386	*Posidonia oceanica*	***Schizophyllum commune***	MF098692	MF115835	--	--	MF136459	MF282007	--	--
MUT 4387	*Posidonia oceanica*	***Schizophyllum commune***	MF098693	MF115834	--	--	MF136460	--	--	--
MUT 4388	*Posidonia oceanica*	***Schizophyllum commune***	KC339233	MF115833	--	--	MF136461	--	--	--
MUT 4875	*Flabellia petiolata*	***Schizophyllum commune***	KX988018§	MF115832	--	--	MF136462	--	--	--
MUT 5200	*Padina pavonica*	***Schizophyllum commune***	KT715697	MF115831	--	--	MF136463	--	--	--
MUT 5204	*Padina pavonica*	***Schizophyllum commune***	KT715698	MF115830	--	--	MF136464	--	--	--
MUT 5240	*Padina pavonica*	***Schizophyllum commune***	KM355991	MF115829	--	--	MF136465	--	--	--
Polyporales										
Bjerkanderaceae										
MUT 2492	*Dysidea fragilis*	***Lopharia spadicea***	MF140468	MF140460	--	--	MF150871	--	--	--
MUT 5195	*Padina pavonica*	***Bjerkandera adusta***	KM355986	MF115840	--	--	MF150867	--	--	--
Irpicaceae										
MUT 2288	*Grantia compressa*	***Ceriporia lacerata***	MF125292	MF125289	--	--	MF150865	MF282005	--	--
MUT 2370	*Dysidea fragilis*	***Irpex lacteus***	MF098696	MF115838	--	--	MF150863	MF282003		--
MUT 2966	*Aplysina cavernicola*	***Irpex lacteus***	MF098695	MF115837	--	--	MF136434	--	--	--
Meruliaceae										
MUT 1939	*Oil splil water*	***Tyromyces fissilis***	KU935697*	MF115839	--	--	MF150866	--	--	--
Polyporaceae										
MUT 2444	*Dysidea fragilis*	***Trametes gibbosa***	MF098690	MF115827	--	--	--	--	--	--
MUT 3263	*Dysidea fragilis*	***Trametes gibbosa***	MF098691	MF115828	--	--	MF136433	MF136440	--	--
Russulales										
Peniophoraceae										
MUT 4993	*Flabellia petiolata*	***Peniophora cinerea***	KR014375§	KP671738§	KT587326§	--	MF150870	--	--	--
MUT 5203	*Padina pavonica*	***Peniophora incarnata***	KM355987	MF125291	--	--	MF150862	--	--	--
Cystobasidiomycetes										
Cystobasidiomycetes incertae sedis										
Buckleyzymaceae										
MUT 5471	*Padina pavonica*	***Buckleyzyma aurantiaca***	MF102877	--	MF112029	KU314991§	MF136428	MF136437	--	--

Microbotryomycetes										
Sporidiobolales										
Sporidiobolaceae										
MUT 73	*Padina pavonica*	***Rhodotorula graminis***	**MF102880**	--	**MF112032**	**KU158181§**	**MF136431**	--	--	--
MUT 2266	*Pachymatisma johnstonia*	***Rhodotorula graminis***	**MF102881**	--	**MF112033**	**MF112036**	**MF136432**	--	--	--
MUT 2415	*Grantia compressa*	***Rhodotorula mucilaginosa***	**MF423718**	--	**MF521972**	**MF521975**	--	--	--	--
MUT 2669	*Posidonia oceanica*	***Rhodotorula diobovata***	**MF102878**	--	**MF112030**	**MF112034**	**MF136429**	**MF136438**	--	--
MUT 4384	*Posidonia oceanica*	***Sporobolomyces roseus***	**MF102879**	--	**MF112031**	**MF112035**	**MF136430**	**MF136439**	--	--
Tremellomycetes										
Holtermanniales										
MUT 2943	*Sycon ciliatum*	***Holtermanniella festucosa***	**MF125294**	--	**MF164047**	**MF196244**	**MF150869**	--	--	--
Ustilaginomycetes										
Ustilaginales										
Ustilaginaceae										
MUT 2264	*Pachymatisma johnstonia*	***Pseudozyma aphidis***	**MF423717**	--	**MF521971**	**MF521974**	--	--	--	--
Wallemiomycetes										
Wallemiales										
Wallemiaceae										
MUT 103	*Padina pavonica*	***Wallemia sebi***	**KT699119**	--	--	--	--	**MF136441**	**MF136443**	**MF136445**
MUT 4935	*Padina pavonica*	***Wallemia sebi***	**MF098689**	--	--	--	--	**MF136442**	**MF136444**	**MF136446**
Additional non marine strains										
MUT 1037	basidiome	***Schizophyllum commune***	**MF423708**	**MF423698**	--	--	**MF977550**	--	--	--
MUT 3331	basidiome	***Schizophyllum commune***	**MF423710**	**MF423700**	--	--	**MF977551**	--	--	--
MUT 3335	basidiome	***Schizophyllum commune***	**MF423711**	**MF423701**	--	--	**MF977552**	--	--	--
MUT 3412	*Carpinus* trunk	***Schizophyllum commune***	**MF423715**	**MF423705**	--	--	**MF977553**	--	--	--
MUT 1585	basidiome	***Lopharia spadicea***	**MF919666**	**MF919668**	--	--	**MF948006**	--	--	--
MUT 3421	dead branch	***Lopharia spadicea***	**MF919667**	**MF919669**	--	--	**MF948007**	--	--	--
LY18491	*Ulex europaeus*	***Porostereum fulvum***	**MG649452**	**MG649454**	--	--	--	--	--	--
LY18496	decaying branch	***Porostereum fulvum***	**MG649453**	**MG649455**	--	--	--	--	--	--

§ sequences obtained by Gnavi et al (2017); * sequence obtained by Bovio et al (2017).

Table 2. Type of datasets used for phylogenetic analyses with number of taxa included, characters of the alignement and support of the resulting phylogram

Family/Order/Class	Dataset	Ingroup taxa	Characters	Number of supported nodes in Bayesian analysis (BPP > 0.70)	Number of supported nodes in ML analysis (BS > 0.5)
Psathyrellaceae	nrITS+nrLSU+*ef-1α*	86	1696 bp	67 (80%)	67 (80%)
Psathyrellaceae (*Coprinellus*)	nrITS+nrLSU	34	1284 bp	29 (85%)	25 (73%)
Schizophyllaceae	nrITS+nrLSU+*ef-1α*	22	1671 bp	8 (36%)	9 (41%)
Phleboid clade of Polyporales	nrITS+nrLSU+*ef-1α*	32	1991 bp	26 (81%)	29 (90%)
Bjerkanderaeae	nrITS+nrLSU	13	1054 bp	11 (85%)	13 (100%)
Polyporaceae	nrITS+nrLSU+*ef-1α*+*rpb1*+*rpb2*	37	3820 bp	35 (95%)	34 (92%)
Russulales (Peniophoraceae)	nrITS	33	480 bp	18 (55%)	21 (63%)
Holtermanniales	nrITS+nrSSU+D1/D2+*ef-1α*	15	2663 bp	10 (67%)	14 (93%)
Ustilaginales	nrITS+nrSSU+D1/D2	40	2231 bp	30 (75%)	26 (65%)
Cystobasidiomycetes-Microbotryomycetes	nrITS+nrSSU+D1/D2+*ef-1α*	86	2743 bp	66 (77%)	71 (83%)
Wallemiaceae	nrITS+*rpb1*+*rpb2*+*tsr1*	39	1733 bp	16 (41%)	25 (64%)

SUPPLEMENTARY MATERIALS

Supplementary Figure S.1. Bayesian phylogram of the genus *Coprinellus* based on a nrITS and nrLSU dataset. The tree is rooted to the gracilis clade of Psathyrellaceae (*Psathyrella bipellis* and *P. corrugis*). Branch numbers indicate BPP values; Bar = expected changes per site (0.02).

Supplementary Figure S.2. Bayesian phylogram of Bjerkanderaceae based on a nrITS and nrLSU dataset. The tree is rooted to Polyporaceae (*Dendrodontia bicolor* and *Dentocorticum sulphurellum*. Branch numbers indicate BPP values; Bar = expected changes per site (0.04).

Supplementary Figure S.3. Bayesian phylogram of Holtermanniales based on a combined nrITS, nrSSU, D1/D2 and *ef-1α* dataset. The tree is rooted to *Filobasidium capsuligenum*. Branch numbers indicate BPP values; Bar = expected changes per site (0.02).

Supplementary Figure S.4. Bayesian phylogram of Ustilaginales based on a combined nrITS, nrSSU and D1/D2 dataset. The tree is rooted to Malasseziomycetes (*Malassezia equina* and *M. caprae*). Branch numbers indicate BPP values; Bar = expected changes per site (0.08).

Supplementary Table S.1. Genbank sequences used for the multilocus phylogenetic analysis of Psathyrellaceae.

TAXON	STRAIN	SUBSTRATE	nrITS	nrLSU	*ef-1α*
Agrocybe praecox	**MSC 378486**	unknown	**AY194531**	**AY207140**	**DQ061276**
Bolbitius vitellinus	**MSC 378484**	unknown	**AY194519**	**AY207147**	**DQ408148**
Bolbitius vitellinus	**AFTOL 730**	grass	**DQ200920**	**AY691807**	**DQ408148**
Conocybe lactea	**AFTOL 1675**	lawn	**DQ486693**	**DQ457660**	--
Coprinellus aureogranulatus	**CBS 973.95**	soil	**GQ249274**	**GQ249283**	**GQ249267**
Co. bisporus	**SZMC-NL-2512**	unknown	**FN396107**	**FN396159**	**FN396215**
	10a2-1-r	*Populus cathayana*	**KT192303**	--	--
Co. brevisetulosus	**SZMC-NL-2908**	unknown	**GU227711**	**JN159585**	--
Co. callinus	**SZMC-NL-1931**	unknown	**FN396105**	**FN396158**	**FN396213**
Co. congregatus	**SZMC-NL-2138**	unknown	**FM878013**	**FM876270**	--
	SZMC-NL-0588	unknown	**JN943129**	**JQ045866**	--
Co. curtus	**SZMC-NL-2339**	unknown	**FM878016**	**FM876273**	**FM897246**
Co. disseminatus	**SZMC-NL-2337**	unknown	**FM878017**	**FM876274**	--
	SZMC-NL-3401	unknown	**JN159561**	**JN159587**	--
Co. radians	**M105**	unknown	**HM595561**	**HM595607**	--
	SZMC-NL-1373	unknown	**JN943118**	**JN159596**	--
Co. flocculosus	**SZMC-NL-1661**	unknown	**FN396138**	**FN396208**	--
Co. heptemerus	**SZMC-NL-2144**	unknown	**FM163178**	**FM160731**	**FM897243**
Co. impatiens	**SZMC-NL-1164**	unknown	**FM163177**	**FM160732**	**FM897261**
Co. pellucidus	**SZMC-NL-2344**	unknown	**FM878023**	**FM876280**	-
Co. sassii	**SZMC-NL-1495**	unknown	**FN396101**	**FN396155**	**FN396210**

Co. truncorum	**SZMC-NL-1294**	unknown	**FM878007**	**FM876263**	**FM897228**
	SZMC-NL-1101	unknown	**FM878006**	**FM876262**	**FM897225**
Co. xanthothrix	**SZMC-NL-1292**	unknown	**FM878008**	**FM876264**	**FM897229**
Coprinopsis atramentaria	**SZMC-NL-4245**	unknown	**FN396123**	**FN396172**	**FN396225**
Cop. calospora	**CBS 612.91**	soil	**GQ249275**	**GQ249284**	**GQ249268**
Cop. candidolanata	**SZMC-NL-2338**	unknown	**FM878002**	**FM876257**	**FM897251**
Cop. cinerea	**SZMC-NL-2141**	unknown	**FN396149**	**FN396190**	**--**
Cop. episcopalis	**SZMC-NL-3032**	unknown	**FN396118**	**FN396200**	**FN396222**
Cop. erythrocephala	**SZMC-NL-4153**	unknown	**FN396125**	**FN396174**	**FN396227**
Cop. gonophylla	**SZMC-NL-0378**	unknown	**FN396147**	**--**	**FN396242**
Cop. insignis	**SZMC-NL-4244**	unknown	**FN396124**	**FN396173**	**FN396226**
Cop. krieglsteinerii	**SZMC-NL-2345**	unknown	**FM878019**	**FM876276**	**--**
Cop. laanii	**CBS 476.70**	unknown	**GQ249276**	**GQ249285**	**--**
Cop. lagopus	**SZMC-NL-2532**	unknown	**FM878031**	**FM876289**	**FM897248**
Cop. macrocephala	**SZMC-NL-1376**	unknown	**FN396126**	**FN396175**	**--**
Cop. marcescibilis	**SZMC-NL-2140**	unknown	**FM878020**	**FM876277**	**FM897257**
Cop. spelaiophila	**SZMC-NL-3031**	unknown	**FN396117**	**FN396167**	**FN396221**
Cop. narcotica	**SZMC-NL-2342**	unknown	**FM163180**	**FM160729**	**FN396244**
Cop. pannucioides	**SZMC-NL-3528**	unknown	**FN396143**	**FN396202**	**FN396238**
Cop. poliomallus	**SZMC-NL-2336**	unknown	**FM163182**	**FM160727**	**FM897244**
Cop. pseudonivea	**SZMC-NL-2340**	unknown	**FM163181**	**FM160728**	**FN430698**
Cop. sclerotiger	**CBS 596.80**	soil	**GQ249277**	**GQ249286**	**GQ249269**
Cop. semitalis	**CBS 291.77**	unknown	**GQ249278**	**GQ249287**	**GQ249270**
Coprinus bellulus	**SZMC-NL-2341**	unknown	**FM163176**	**FM160680**	**--**
Coprinus cortinatus	**SZMC-NL-1621**	unknown	**FN396121**	**FN396171**	**FN396224**
Coprinus coniophorus	**SZMC-NL-3414**	unknown	**FN396122**	**FN396207**	**--**
Coprinus patouillardii	**SZMC-NL-1687**	unknown	**FM878009**	**FM876265**	**FM897238**
Coprinus utrifer	**SZMC-NL-0591**	unknown	**FN396140**	**FN396209**	**--**
Lacrymaria glareosa	**WU 16293**	unknown	**HQ872015**	**HQ847134**	**HQ847208**
L. lacrymabunda	**SZMC-NL-2140**	unknown	**FM163184**	**FM160725**	**FN430688**
L. pyrotricha	**CBS 573.79**	unknown	**GQ249280**	**GQ249289**	**GQ249272**
L. velutina	**AFTOL 478**	unknown	**DQ490639**	**AY700198**	**--**
Parasola auricoma	**SZMC-NL-0087**	unknown	**FM163185**	**FM160724**	**FM897236**
Pa. conopilus	**SZMC-NL-0285**	unknown	**FM163225**	**FM160684**	**FM897237**
Pa. leiocephala	**SZMC-NL-0466**	unknown	**FM163192**	**FM160717**	**FM897241**
Pa. lilatincta	**SZMC-NL-0660**	unknown	**FM163195**	**FM160714**	**FM897230**
Pa. megasperma	**SZMC-NL-1924**	unknown	**FM163208**	**FM160701**	**FM897232**
Pa. misera	**SZMC-NL-0667**	unknown	**FM163211**	**FM160698**	**FM897240**
Pa. plicatilis	**SZMC-NL-0287**	unknown	**FM163212**	**FM160697**	**--**
Psathyrella ammophila	**SZMC-NL-2151**	unknown	**FM163220**	**FM160689**	**FM897260**
Ps. badiophylla	**SZMC-NL-2347**	unknown	**FN430699**	**FM876268**	**FM897252**
Ps. bipellis	**SZMC-NL-0638**	unknown	**FN430700**	**FN396160**	**FN396216**
Ps. candolleana	**AFTOL 1507**	unknown	**DQ494689**	**DQ110874**	**--**
Ps. candolleana	**SZMC-NL-2145**	unknown	**FM878001**	**FM876256**	**--**
Ps. candolleana	**SZMC-NL-2937**	unknown	**FN396114**	**FN396165**	**FN396220**
Ps. corrugis	**SZMC-NL-3395**	unknown	**FN430692**	**FN396205**	**FN396240**
Ps. fatua	**SZMC-NL-0603**	unknown	**FN396142**	**FN396201**	**FN396237**
Ps. fibrillosa	**SZMC-NL-0201**	unknown	**FN396137**	**FN396181**	**FN396232**
Ps. fusca	**SZMC-NL-0630**	unknown	**FM878021**	**FM876278**	**FM897256**
Ps. leucotephra	**SZMC-NL-1953**	unknown	**FM163226**	**FM160683**	**FM897219**
Ps. magnispora	**SZMC-NL-1954**	unknown	**FM163227**	**FM160682**	**FM897218**
Ps. microrhiza	**SZMC-NL-3059**	unknown	**FN396130**	**FN396178**	**FN396230**
Ps. noli-tangere	**SZMC-NL-3403**	unknown	**FN396144**	**FN396203**	**FN396239**
Ps. pertinax	**SZMC-NL-2350**	unknown	**FM878012**	**FM876269**	**FM897259**
Ps. phegophila	**SZMC-NL-3527**	unknown	**FN396129**	**FN396198**	**FN396229**
Ps. piluliformis	**SZMC-NL-3923**	unknown	**FN396136**	**FN396185**	**FN396235**
Ps. pygmaea	**SZMC-NL-2325**	unknown	**FM878011**	**FM876267**	**FM897224**
Ps. spadicea	**SZMC-NL-3450**	unknown	**FN396134**	**FN396183**	**FN396180**
Ps. spadiceogrisea	**SZMC-NL-0440**	unknown	**FM878024**	**FM876282**	**FM897223**
Ps. umbrina	**SZMC-NL-1949**	unknown	**FM878004**	**FM876260**	**FM897226**
Additional taxa for *Coprinellus*					
Co. amphitallus	**L128**	unknown	**HQ846978**	**HQ847065**	**--**
Co. bisporiger	**SZMC-NL-3856**	unknown	**HQ846976**	**HQ847063**	**--**
Co. bisporus	**SZMC-NL-0158**	unknown	**GU227705**	**HQ847062**	**--**
Co. canistri	**Walleyn 877**	unknown	**HQ846985**	**--**	**--**

Co. heterosetulosus	**SZMC-NL-1059**	unknown	**GU227708**	**HQ847075**	--
Co. marculentus	**SZMC-NL-1167**	unknown	**GU227706**	**HQ847089**	--
Co. micaceus	**SZMC-NL-3656**	unknown	**JN159567**	**JN159588**	--
Co. pallidus	**SZMC-NL-1556**	unknown	**HQ846989**	**HQ846989**	--
Co. plagiosporus	**SZMC-NL-1365**	unknown	**HQ846981**	**HQ847068**	--
Co. radicellus	**SZMC-NL-3168**	unknown	**GU227719**	**HQ847077**	--
Co. sclerocystidiosus	**SZMC-NL-1018**	unknown	**HQ846991**	**HQ847079**	--
Co. rufopruinatus	**SZMC-NL-1939**	unknown	**FN396104**	**FN396157**	--

Supplementary Table S.2. Genbank sequences used for the multilocus phylogenetic analysis of Schizophyllaceae.

TAXON	STRAIN	SUBSTRATE	nrITS	nrLSU	*ef-1α*
S. commune	**CBS 132304**	clinical patient	**LT217530**	**LT217561**	**LT217595**
	CBS 476.64	unknown	**LT217531**	**LT217562**	**LT217596**
	MUCL 30748	*Saccharum officinarum*	**LT217534**	**LT217566**	**LT217600**
	MUCL 31016	Hay	**LT217535**	**LT217567**	**LT217601**
S. radiatum	**CBS 301.32**	unknown	**LT217537**	**LT217569**	**LT217603**
	UTHSCSA DI14-1	unknown	**LT217539**	**LT217571**	**LT217605**
	UTHSCSA DI14-8	unknown	**LT217543**	**LT217577**	**LT217611**
	UTHSCSA DI14-10	unknown	**LT217545**	**LT217579**	**LT217613**
S. fasciatum	**CBS 267.60**	unknown	**LT217559**	**LT217593**	**LT217627**
S. umbrinum	**MUCL 43017**	unknown	**LT217560**	**LT217594**	**LT217628**

Supplementary Table S.3. Genbank nrITSsequences used for the phylogenetic analysis of Peniophoraceae.

TAXON	STRAIN	SUBSTRATE	nrITS
Amanita citrina	**TENN61704**	unknown	**FJ596867**
Amanita rubescens	**MC01-556**	sporocarp	**AJ889922**
Peniophora albobadia	**LPSC-285**	unknown	**KU530154**
Peniophora aurantiaca	**FCUG 2563**	unknown	**AF210825**
Peniophora aurantiaca	**FCUG 0682**	unknown	**AF210827**
Peniophora aurantiaca	**NH6666**	unknown	**AF210829**
Peniophora* cf. *limitata	**UC2022878**	litter	**KP814438**
Peniophora cinerea	**V1M4F82**	wheat plant	**KT692548**
Peniophora cinerea	**P.CH-13**	wood	**KF562015**
Peniophora crassitunicata	**JSP 02 A 5**	nest of *Atta capiguara*	**KR093906**
Peniophora incarnata	**NH10271**	unknown	**AF506425**
Peniophora incarnata	**olrim391**	*Picea abies*	**AY781263**
Peniophora incarnata	**F35-1**		**JF439504**
Peniophora incarnata	**OK-RAW-5**	wood pellets	**KX766174**
Peniophora incarnata	**olrim190**	*Picea abies*	**AY805616**
Peniophora laxitexta	**LGMF1159**	Leaves of *Vochysia divergens*	**JX559580**
Peniophora laxitexta	**BAFC 3309**	unknown	**FJ882040**
Peniophora lycii	**2142**	unknown	**JX046435**
Peniophora nuda	**AFTOL-ID 660**	unknown	**DQ411533**
Peniophora piceae	**209**	bottom sediment of bog	**JX507718**
Peniophora piceae	**olrim10**	Picea abies	**AY781264**
Peniophora piceae	**OK-RAW-8**	wood pellets	**KX766177**
Peniophora piceae	**olrim883**	*Picea abies*	**AY805634**

Peniophora pini	**KuP8**	*Pinus contorta* var. *latifolia*	**KP698183**
Peniophora pini	**Hjm 18143**	unknown	**EU118651**
Peniophora pithya	**TPPtB1012**	unknown	**AF119520**
Peniophora pithya	**CEQCA-I1332**	*Siphocampylus* sp. Pohl	**KC771449**
Peniophora pseudo-pini	**TPPpB1007**	unknown	**AF119514**
Peniophora rufa	**TPRuB1014**	unknown	**AF119516**
Phlebiopsis gigantea	**A-P011**	unknown	**AF087487**
Phlebiopsis gigantea	**C-P160**	unknown	**AF087488**
Phlebiopsis gigantea	**UASWS0307**	forest soil	**EF174446**
Phlebiopsis gigantea	**ZS2**	unknown	**JX946673**

Supplementary Table S.4. Genbank sequences used for the multilocus phylogenetic analysis of the Phleboid clade of Polyporales.

TAXON	STRAIN	SUBSTRATE	nrITS	nrLSU	*ef-1α*
Antrodiella americana	**3161**	unknown	**JN710509**	**JN710509**	**JN710711**
A. faginea	**3165**	unknown	**JN710514**	**JN710514**	**JN710712**
Bjerkandera adusta	**MT 49214**	unknown	**KT305935**	**KT305935**	**KT305938**
	MT 482014	unknown	**KT305936**	**KT305936**	--
	SFC20111029-15	unknown	**KJ704813**	**KJ704828**	--
B. atroalba	**VMV 216**	unknown	**KT305931**	**KT305931**	**KT305939**
	VMV 158	unknown	**KT305932**	**KT305932**	**KT305940**
B. centroamericana	**JK0610/A7**	unknown	**KT305933**	**KT305933**	**KT305941**
	JK9610/A13	unknown	**KT305934**	**KT305934**	**KT305942**
Bjerkandera fumosa	**SFC20121009-04**	unknown	**KJ704824**	**KJ704839**	--
Ceriporia lacerata	**NIBRFG0000114712**	unknown	**JN641761**	**JN641759**	--
C. reticulata	**KHL 11981**	unknown	**JX109845**	**EU118614**	**JX109899**
Climacodon septentrionalis	**AFTOL 767**	acer	**AY854082**	**AY684165**	**AY885151**
Gleoporus taxicola	**SK 0075**	unknown	**JX109847**	**JX109847**	**JX109901**
Heterobasidion annosum	**AFTOL 470**	xylem	**JF440572**	--	**DQ028583**
Junghuhnia nitida	**3135**	unknown	**JN710560**	**JN710560**	**JN710721**
Ischnoderma resinosum	**CIRM-BRFM 955**	unknown	**GU731564**	**AJ487927**	--
Irpex lacteus	**DO 421/951208**	unknown	**JX109852**	**JX109852**	**JX109911**
Mycoacia fuscoatra	**KHL13275**	unknown	**JN649352**	**JN649352**	**JX109908**
Phanerochaete chrysosporium	**BKM-F-1767**	unknown	**HQ188436**	**GQ470643**	**HQ188379**
Ph. sordida	**KHL 12054**	unknown	**EU118653**	**EU118653**	--
Phlebia nitidula	**20830**	unknown	**EU118655**	**EU118655**	--
P. radiata	**AFTOL 484**	unknown	**AY854087**	**AF287885**	**AY885156**
Trametopsis cervina	**TJV 93 216**	unknown	**JN165020**	**JN164796**	**JN164882**
Tyromyces fissilis	**814**	acer campestre	**HQ728291**	**HQ729001**	--
	BRNM 699803	populus tremula	**HQ728292**	**HQ729002**	--

Supplementary Table S.5. Genbank sequences used for the multilocus phylogenetic analysis of Polyporaceae.

TAXON	STRAIN	SUBSTRATE	nrITS	nrLSU	*rpb1*	*rpb2*	*ef-1α*
Coriolopsis polyzona	**BKW-004**	unknown	**JN164978**	**JN164790**	**JN164844**	**JN164856**	**JN164881**
	OH272sp	unknown	**JN164979**	--	--	--	--
Lenzites betulinus	**HHB-9942-Sp**	unknown	**JN164983**	**JN164794**	**JN164822**	**JN164860**	**JN164895**
	DSH97	unknown	**KF573021**	--		**KF573147**	**KF573092**
Lopharia cinerascens	**FP-105043-sp**	unknown	**JN165019**	**JN164813**	**JN164840**	**JN164874,**	**JN164900**
Pycnoporus cinnabarinus	**ZW 02-30**	unknown	**DQ411525**	**AY684160**	**JN164843**	**DQ408121**	**DQ02860**

	PR-SC-95	unknown	**JN164982**	**JN164795**	**JN164842**	**JN164858**	**JN164897**
Trametes aff. maxima	**FPRI-401**	unknown	**JN164933**	**JN164802**	**JN164836**	**JN164863**	**JN164884**
Trametes conchifer	**FP-106793**	unknown	**JN164924**	**JN164797**	**JN164823**	**JN164849**	**JN164887**
	FP-86583-R	unknown	**JN164939**	**--**	**--**	**KF573095**	**KF573038**
Trametes cubensis	**AJ177**	unknown	**JN164905**	**JN164787**	**--**	**--**	**--**
	TJV-93-213	unknown	**JN164923**	**JN164798**	**JN164834**	**JN164865**	**JN164883**
Trametes ectypa	**FP-81034-R**	unknown	**JN164930**	**--**	**KF573149**	**KF573094**	**KF573041**
	FP-106037-T	unknown	**JN164929**	**JN164803**	**JN164824**	**JN164848**	**JN164888**
Trametes elegans	**FRI-437-T**	unknown	**JN164985**	**--**	**KF573177**	**KF573142**	**KF573080**
	FP-105679-Sp	unknown	**JN164944**	**JN164799**	**JN164833**	**JN164861**	**JN164899**
Trametes gibbosa	**L-11664-Sp**	unknown	**JN164943**	**JN164800**	**JN164831**	**JN164859**	**JN164896**
	DMC815	unknown	**KC589144**	**KC589164**	**--**	**--**	**--**
Trametes hirsuta	**AJ196**	unknown	**JN164916**	**--**	**--**	**KF573125**	**KF573071**
	RLG-5133-T	unknown	**JN164941**	**JN164801**	**JN164829**	**JN164854**	**JN164891**
Trametes maxima	**OH-189-Sp**	unknown	**JN164957**	**JN164804**	**JN164816**	**JN164864**	**JN164885**
Trametes membranacea	**PR-3264**	unknown	**JN164946**	**--**	**KF573169**	**KF573132**	**KF573084**
	PR-SC-82	unknown	**JN164945**	**JN164805**	**JN164832**	**JN164857**	**JN164893**
Trametes ochracea	**MJL-2103**	unknown	**JN164948**	**--**	**KF573158**	**KF573121**	**KF573056**
	HHB-13445-Sp	unknown	**JN164954**	**JN164812**	**JN164826**	**JN164852**	**JN164904**
Trametes pavonia	**FP-103050-Sp**	unknown	**JN164958**	**JN164806**	**JN164835**	**JN164862**	**JN164886**
Trametes pocas	**Dai11577**	unknown	**KC848253**	**KC848340**	**--**	**--**	**--**
Trametes pubescens	**L-15318-Sp**	unknown	**JN164949**	**--**	**KF573162**	**KF573113**	**KF573064**
	FP-101414-Sp	unknown	**JN164963**	**JN164811**	**JN164827**	**JN164851**	**JN164889**
Trametes suaveolens	**HHB-14170-T**	unknown	**JN164968**	--	**KF573167**	**KF573128**	**KF573066**
	FP-102529-Sp	unknown	**JN164966**	**JN164807**	**JN164828**	**JN164853**	**JN164890**
Trametes versicolor	**AJ146**	unknown	**JN164912**	**--**	**KF573152**	**KF573107**	**KF573048**
	FP-135156-Sp	unknown	**JN164919**	**JN164809**	**JN164825**	**JN164850**	**JN164878**
Trametes villosa	**FP-86588-Sp**	unknown	**JN164970**	--	**--**	**KF573127**	**KF573073**
	FP-71974-R	unknown	**JN164969**	**JN164810**	**JN164830**	**JN164855**	**JN164892**
Dentocorticium sulphurellum	**FP-11801**	unknown	**JN165018**	--	**JN164841**	**JN164876**	**JN164903**

29

30 **Supplementary Table S.6. Genbank sequences used for the multilocus phylogenetic analysis of**
31 **Microbotryomycetes and Cystobasidiomycetes.**

TAXON	STRAIN	SUBSTRATE	nrITS	D1/D2 (nrLSU)	nrSSU	*ef-1α*
Agaricostilbomycetes						
Agaricostilbales						
S. clavatus	**AS 2.2318**	*Sorbus pohuashanensis*	**AY364839**	**AY364839**	**KJ708406**	**KJ707894**
S. diospyroris	**JCM 12157**	leaf of *Diospyros morrisiana*	**AB126047**	**--**	**AB124560**	**KJ707904**
S. lactophilus	**CBS 7527**	dead branch of *Abies firma*	**AF444545**	**AF177411**	**AB021675**	**KJ707889**
S. pyrrosiae	**JCM 12159**	leaf of *Pyrrosia lingua*	**AB126045**	**AB124562**	**AB126045**	**KJ707903**
S. sasicola	**CBS 7285**	dead leaf of *Sasa* sp.	**AF444548**	**AF177412**	**AB021688**	**KJ707900**
S. taupoensis	**CBS 7898**	dead leaf of *Nothofagus fusca*	**AF444592**	**AF177413**	**D66886**	**KJ707901**
S. xanthus	**CBS 7513**	dead leaf of *Acer rufinerve*	**AF444547**	**AF177414**	**D64118**	**KJ707902**
Spiculogloelaes						
S. coprosmicola	**JCM 8767**	leaf of *Coprosma tenuifolia*	**AF444576**	**AF189981**	**D66879**	**KJ707908**
S. dimmenae	**JCM 8762**	leaf of *Pseudowintera colorata*	**AB038046**	**AB644404**	**D66881**	**KJ707907**
S. linderae	**CBS 7893**	dead leaf of *Lindera obtusiloba*	**AF444582**	**AF189989**	**D66885**	**KJ707906**
S. novozealandicus	**JCM 8756**	leaf of *Pseudowintera colonata*	**AB038048**	**KJ708467**	**KJ708443**	**KJ707851**
S. subbrunneus	**CBS 7196**	dead leaf of *Oryza sativa*	**AF444549**	**AF189997**	**AB021691**	**KJ707909**
Cystobasidiomycetes						
Cystobasidiales						
R. minuta	**CBS 319**	air	**AF190011**	**AF189945**	**D45367**	**KJ707825**
R. slooffiae	**CBS 5706**	throat swab	**AF444627**	**AF444722**	**AB126653**	**KJ707828**
Aurantiaca clade *i.s.*						
R. armeniaca	**JCM 8977**	leaf of *Callistemon viminalis*	**AF444523**	**AF189920**	**AB126644**	**KJ707762**
R. aurantiaca	**CBS 317**	air	**AF444538**	**AF189921**	**KJ708436**	**AF444538**

S. kluyveri-nielii	**CBS 7168**	leaf of *Dombeya rotundifolia*	**AF444544**	**AF189988**	**AB021674**	**KJ707760**
S. phyllomatis	**CBS 7198**	leaf of *Dombeya rotundifolia*	**AF444515**	**AF189991**	**AB021685**	**KJ707761**
S. salicinus	**CBS 6983**	leaf of *Salix* sp.	**AF444511**	**AF189995**	**AB021687**	**KJ707758**
S. gracilis	**CBS 71**	decaying leaves	**AF444578**	**AF189985**	**KJ708433**	**KJ707799**
R. marina	**CBS 2365**	shrimp	**AF444504**	**AF189944**	**AB126645**	**KJ707795**
S. symmetricus	**CBS 9727**	Siberian silver birch	**AY364836**	**AY364836**	**KJ708350**	**KJ707800**
S. vermiculatus	**JCM 10224**	Leaf of *Pennisetum pedicellatum*	**AB030335**	**AF460176**	**AB030322**	**KJ707801**
Sakaguchia clade *i.s.*						
R. cladiensis	**CBS 10878**	headwaters	**FJ008055**	**FJ008049**	**KJ708354**	**KJ707847**
R. oryzicola	**AS 2.2363**	unknown	**AY335160**	**AY335161**	**KJ708352**	**KJ707853**
R. oryzicola	**AS 2.3289**	unknown	**KP216523**	**KJ708451**	**KJ708353**	**KJ707848**
Microbotryomycetes						
R. arctica	**CBS 9278**	soil	**AB478857**	**AB478858**	**KJ708371**	**KJ707856**
R. auriculariae	**CBS 6379**	basidiome of *Auricularia auricula-judae*	**AF444507**	**AF189922**	**KJ708429**	**KJ707935**
R. cresolica	**CBS 7998**	soil contaminated with orthocresol	**AF444570**	**AF189926**	**KJ708365**	**KJ707942**
R. diffluens	**CBS 5233**	leaf of *Tillandsia usneoides*	**AF444533**	**AF075485**	**KJ708380**	**KJ707939**
S. falcatus	**CBS 7368**	dead leaf of *Miscanthus sinensis*	**AF444543**	**AF075490**	**AB021670**	**KJ707943**
R. hordea	**AFTOL 674**	leaf of *Hordeum hexastichon*	**AF444524**	**AF189933**	**AY657013**	**KJ707802**
R. hylophila	**CBS 6226**	tunnel of *Xyleborus aemulus*	**AF444622**	**AF363645**	**KJ708431**	**KJ708236**
Kriegeriales						
R. glacialis	**CBS 10436**	glacier cryoconite	**EF151249**	**EF151258**	**KJ708381**	**KJ707831**
R. psychrophenolica	**CBS 10438**	mud at the glacier foot	**EF151246**	**EF151255**	**KJ708382**	**KJ707859**
R. rosulata	**CBS 10977**	dead pine needles	**EU872492**	**EU872490**	**KJ708384**	**KJ707854**
Buffoni clade *i.s.*						
R. buffonii	**CBS 2838**	*Boletus edulis* var. *albus*	**AF444526**	**AF189924**	**KJ708362**	**KJ707946**
R. bogoriensis	**CBS 4101**	leaf of *Randia malleifera*	**AF444536**	**AF189923**	**KJ708363**	**KJ707949**
R. pustula	**CBS 6527**	fruit of *Ribes nigrum*	**AF444531**	**AF189964**	**KJ708361**	**KJ707937**
Calacogloea clade i.s.						
R. cycloclastica	**CBS 8448**	soil	**AF444732**	**AF444631**	**KJ708376**	**KJ707775**
R. eucalyptica	**CBS 8499**	unknown	**EU075185**	**EU075183**	**KJ708377**	--
R. philyla	**CBS 6272**	tunnel of *Xyleborus ferrugineus*	**AF444506**	**AF075471**	**KJ708438**	**KJ707772**
R. retinophila	**CBS 8446**	soil	**AF444624**	**AF444730**	**KJ708373**	**KJ707771**
R. terpenoidalis	**CBS 8445**	soil	**AF444623**	**AF444729**	**KJ708374**	**KJ707774**
Tsugae clade *i.s.*						
R. pilati	**CBS 7039**	litter of *Abies alba*	**AF444598**	**AF189963**	**KJ708364**	**KJ707947**
S. tsugae	**CBS 5038**	*Tsuga heterophylla*	**AF444580**	**AF189998**	**AB021692**	**KJ707945**
Yarrowii clade *i.s.*						
R. silvestris	**CBS 11420**	dead needles of *Picea abies*	**GQ121045**	**GQ121044**	**KJ708366**	**KJ707849**
R. straminea	**CBS 10976**	dead pine needles	**EU872491**	**EU872489**	**KJ708367**	**KJ707844**
R. yarrowii	**CBS 7417**	decaying mushroom	**AF444628**	**AF189971**	**AB032658**	**KJ707938**
Sporidiobolales						
R. araucariae	**CBS 6031**	rotting bark of *Araucaria araucana*	**AF444510**	**AF070427**	**KJ708435**	**KJ707862**
R. diobovata	**CBS 6085**	sea water	**AF444502**	**AF070421**	**AB073271**	**KJ707865**
R. glutinis	**CBS 20**	air	**AF444539**	**AF070429**	**X69853**	**KJ707869**
R. graminis	**CBS 2826**	grass	**AF444505**	**AF070431**	**X83827**	**KJ707868**
R. kratochvilovae	**CBS 7436**	unknown	**AF444520**	**AF071436**	**AB073273**	**KJ707863**
R. mucilaginosa	**JCM 8115T**	unknown	**AF444541**	**AF070432**	**AB021668**	**KJ707861**
R. pacifica	**CBS 10070**	deep-sea sediment	**AB026006**	**AB026006**	**KJ708397**	**KJ707860**
R. sphaerocarpa	**CBS 5939**	Anctarctic sea	**AF444499**	**AF070425**	**AB073275**	**KJ707867**
R. taiwanensis	**CBS 11729**	*Artemisia princeps*	**GU646862**	**GU646863**	**KJ708409**	**KJ707838**
R. azoricum	**JCM 11251**	soil	**AB073229**	**AF321977**	**AB073269**	**KJ707813**
R. colostri	**CBS 348**	Human colostrum	**JN246563**	**AY372177**	**KJ708399**	**KJ707818**
R. fluviale	**CBS 6568**	brackish water	**AY015432**	**AF189915**	**AB073272**	**KJ707816**
R. lusitaniae	**CBS 7604**	soil of woodland	**AY015430**	**AF070423**	**AB073274**	**KJ707812**
S. microsporus	**CBS 7041**	herbaceous culm	**AF444535**	**AF070436**	**KJ708441**	**KJ707817**
S. nylandii	**JCM 10213**	leaf of *Oryza sativa*	**AB030323**	**AF387123**	**AB030319**	**KJ707822**
S. odoratus	**JCM 11641**	basidiome of *Myxarium nucleatum*	**KJ778638**	**AF387125**	**KJ708427**	**KJ707819**
S. poonsookiae	**JCM 10207**	leaf of *Mangifera indica*	**AB030327**	**AF387124**	**AB030320**	**KJ707821**
S. ruineniae	**CBS 5811**	dung of goat	**AF444491**	**AF070434**	**AB021693**	**KJ707820**

S. blumeae	**JCM 10212**	leaf of *Blumea* sp.	**AB030331**	**AY213010**	**AB030321**	**KJ707926**
S. carnicolor	**JCM 3766**	unknown	**AY069991**	**AY070008**	**KJ708434**	**KJ707912**
S. johnsonii	**CBS 5470**	leaf of *Rubus*	**AY015431**	**AF070435**	**L22261**	**KJ707914**
S. johnsonii	**CBS 1522**	fodder yeast	**AF444509**	**AF189975**	--	**KJ707916**
S. longiusculus	**CBS 9655**	subsurface water	**JN246566**	**KJ708464**	**KJ708400**	**KJ707929**
S. metaroseus	**CBS 7683**	plant	**EU003482**	**EU003461**	**KJ708415**	**KJ707841**
S. patagonicus	**CBS 9658**	subsurface water	**AY552329**	**AY158656**	**KP216518**	**KJ707930**
S. phaffii	**AS 2.2137**	dead leaf of *Nerium indicum*	**AY069995**	**AY070011**	**KJ708404**	**KJ707918**
S. roseus	**CBS 486**	unknown	**AY015438**	**AF070441**	**X60181**	**KJ707917**
S. ruberrimus	**CBS 7550**	soil	**AY015439**	**AF070442**	**KJ708402**	**KJ707915**
S. salmonicolor	**CBS 490**	unknown	**AY015434**	**AF070439**	**AB021697**	**KJ707923**
Ustilagomycotina						
M. phylloplanum	**CBS 8073**	leaf of *Banksia collina*	**AF190004**	**AB038131**	**AJ496258**	**KP323116**
M. phylloplanum	**JCM 9035**	leaf of *Banksia collina*	**AB038131**	**AF190004**	**AJ496258**	--

Supplementary Table S.7. Genbank sequences used for the multilocus phylogenetic analysis of Holtermanniales.

TAXON	STRAIN	SUBSTRATE	nrITS	D1D2 (nrLSU)	nrSSU	*ef-1α*
Holtermanniella festucosa	**CBS 10162**	*Festuca valesiaca*	**KY102693**	**KY107040**	**KF036633**	**KF037052**
	PTZ 53	unknown	**AY633979**	**AY661812**	--	--
	PTZ 31A	unknown	**AY633978**	**AY661811**	--	--
H. mycelialis	**CBS 7712**	soil-Antartica	**AF408417**	**AJ311450**	**KF036641**	**KF037073**
	CBS 7713	soil-Antartica	**AF408418**	**AJ311451**	--	--
	CBS 7743	plant-Antartica	**AF408419**	**AJ311452**	--	--
H. nyarrowii	**CBS 8804**	bird-Antartica	**KY103594**	**AY006480**	**KF036643**	**KF037075**
	CBS 8805	soil-Antartica	**KY103593**	**KY107872**	--	--
H. wattica	**CBS 9496**	soil-Antartica	**NR_138371**	**KY107874**	**KF036662**	**KF037099**
	DBVPG 10591	forest soil	**KU745362**	**KU745305**	--	--
H. takashimae	**CBS 11174**	litter	**NR_137721**	**FM242574**	**KF036679**	**KF037163**
	HB 982	litter	**FM246501**	**FN430735**	--	--
Holtermannia corniformis	**CBS 6979**	unknown	**AF410472**	**AF189843**	**AF053718**	**KF037162**
	CBS 7675	dead wood	**GU937756**	**GU937761**	--	--
	CBS 1906	sake-moto	**AF444381**	**AF363642**	**AB075544**	**KF037152**

Supplementary Table S.8. Genbank sequences used for the multilocus phylogenetic analysis of Ustilaginales.

TAXON	STRAIN	SUBSTRATE	nrITS	D1/D2 (nrLSU)	nrSSU
Malasseziomycetes					
Malassezia caprae	**CBS 10434**	goat	**AY743656**	**KF706456**	**AY743656**
Malassezia equina	**CBS 9969**	horse	**KF706439**	**AY743621**	**KF706454**
Urocystales					
Urocystis colchici	**AFTOL 1647**	unknown	**DQ839596**	**DQ838576**	**DQ839595**
Urocystis eranthidis	**HMK 292**	unknown	**JN367299**	**JN367324**	**JN367352**
Ustilaginales					
Macalpinomyces eriachnes	**CBS 131454**	*Eriachne sulcate*	**JN367287**	**JN367312**	**JN367340**
Melanopsichium pennsylvanicum	**UMa7041**	unknown	**JN367288**	**JN367313**	**JN367341**
Moesziomyces bullatus	**AFTOL 1820**	*Pennisetum typhoideum*	**DQ831013**	**DQ831011**	**DQ831012**
Pseudozyma abaconensis	**CBS 8380**	sea water	**FJ008053**	**FJ008047**	**KP322956**
Pseudozyma antarctica	**JCM 10317**	lake sediment - Antarctica	**JN942668**	**JN940521**	**JN940463**
Pseudozyma antarctica	**CBS 5955**	soil - Antarctica	**AB089358**	**AJ235302**	**KP322960**
Pseudozyma aphidis	**JCM 10318**	aphid secretion	**AB089362**	**AB089363**	**JN940465**
Pseudozyma aphidis	**CBS 517.83**	aphid secretion	**AF294699**	**AJ235303**	--
Pseudozyma aphidis	**CNm2012**	unknown	**KF443199**	**KF443201**	**KF443200**
Pseudozyma flocculosa	**AFTOL 864**	*Secale cereale*	**DQ411535**	**AY745712**	**DQ092923**
Pseudozyma flocculosa	**CBS 167.88**	unknown	**AF294690**	**AJ235299**	**AF294717**
Pseudozyma hubeiensis	**CGMCC 2.2493**	wastewater	**DQ008954**	**DQ008953**	**KP322957**

Pseudozyma prolifica	**JCM 10319**	*Scirpus microcarpus*	**AB089368**	**AB089369**	**--**
Pseudozyma prolifica	**CBS 319.87**	*Scirpus microcarpus*	**AF294700**	**AJ235298**	**AF294724**
Pseudozyma pruni	**BCRC 34227**	*Prunus mume*	**NR_137557**	**EU379943**	**--**
Pseudozyma pruni	**CBS 10937**	*Prunus mume*	**EU379942**	**EU379943**	**KP322958**
Pseudozyma parantarctica	**JCM 11752**	human blood	**JN942671**	**--**	**JN940457**
Pseudozyma parantarctica	**CBS 10005**	human blood	**AB089356**	**AB089357**	**JN940457**
Pseudozyma rugulosa	**CBS 170.88**	mouldy leaf	**AF294697**	**AJ235300**	**--**
Pseudozyma rugulosa	**JCM 10323**	*Zea mays*	**JN942670**	**JN940523**	**JN940458**
Pseudozyma shanxiensis	**AS 2.2523**	*Quercus mongolica*	**DQ008956**	**DQ008955**	**KP866247**
Pseudozyma thailandica	**CBS 10006**	human blood	**AB089354**	**AB089355**	**KP322959**
Sporisorium andropogonis	**CBS 192.26**	*Psidium guajava*	**AY740042**	**AY740095**	**KP322962**
Sporisorium exsertum	**KVU 9651**	unknown	**JN367293**	**JN367318**	**JN367347**
Sporisorium reilianum	**CBS 131460**	*Zea mays*	**KF706438**	**KF706430**	**KF706441**
Sporisorium scitamineum	**CBS 131463**	*Saccharum sp.*	**JN367296**	**JN367321**	**KP322965**
Cintractia sorghi-vulgaris	**AFTOL 867**	unknown	**DQ200931**	**AY745726**	**DQ234548**
Tranzscheliella hypodytes	**RK0741**	unknown	**JN367298**	**JN367323**	**JN367351**
Tranzscheliella williamsii	**CBS 131475**	unknown	**JN367310**	**JN367338**	**KP322974**
Ustilago cynodontis	**MS 1**	*Cynodon dactylon*	**AY740168**	**AY740168**	**JN367355**
Ustilago hordei	**CBS 131470**	*Hordeum vulgare*	**KF706437**	**KF706429**	**KP322978**
Ustilago hordei	**DB 1526**	unknown	**JN367303**	**JN367329**	**JN367357**
Ustilago tritici	**AFTOL 1398**	unknown	**DQ846894**	**DQ094784**	**DQ846895**
Ustilago maydis	**CBS 504.76**	*Zea mays*	**AY854090**	**AF453938**	**KP322979**
Ustilago xerochloae	**KVU 10001**	unknown	**JN367311**	**JN367339**	**JN367362**

Supplementary Table S.9. Genbank sequences used for the multilocus phylogenetic analysis of Wallemiales.

TAXON	STRAIN	SUBSTRATE	nrITS	*tsr1*	*rbp1*	*rbp2*
W. sebi	**CBS 818.96NT**	Sunflower seed	**AY328915**	**KM035026**	**KM035115**	**KM035204**
	CBS 110595	Domestic interior, dormitory	**AY302511**	**KM035073**	**KM035162**	**KM035250**
	CBS 200.33	Unknown	**AY302519**	**KM196459**	**KM196359**	**KM196408**
	EXF-1441	Unknown	**KJ494640**	**KM196417**	**KM196323**	**KM196369**
	EXF-1442	Unknown	**KJ494643**	**KM196418**	**KM196324**	**KM196370**
	MUCL 46253d	Flavoured mineral water	**KJ494638**	**KM196443**	**KM196344**	**KM196397**
	CBS 136843	Archive	**KJ409909**	**KM035063**	**KM035152**	**KM035240**
	CBS 136845	Office building	**KJ409911**	**KM035065**	**KM035154**	**KM035242**
	CBS 136847	Boiled eggs plant	**KJ409913**	**KM035067**	**KM035156**	**KM035244**
	EXF-8748	Office dust	**KJ409896**	**KM035045**	**KM035134**	**KM035223**
	EXF-5746	Hypersaline water of saltern	**KJ494642**	**KM196429**	**KM196335**	**KM196382**
	CBS 110582a	Hypersaline water of saltern	**AY302499**	**KM196448**	**KM196319**	**KM196401**
	CBS 110600	Hypersaline water of Dead Sea	**AY302513**	**KM196454**	**KM196354**	**KM196405**
	CBS 202.33	Sea salt	**AY328912**	**KM196453**	**KM196353**	**KM196404**
	EXF-5860	Hypersaline water of solar saltern	**KJ494636**	**KM196435**	–	**KM196387**
W. mellicola	**CBS 110593**	Straw hat	**AY302509**	**KM196464**	**KM196318**	**KM196413**
	EXF-8741	Dust in house	**KJ409883**	**KM035030**	**KM035119**	**KM035208**
	EXF-8747	House dust	**KJ409895**	**KM035044**	**KM035133**	**KM035222**
	DAOM 242696	Dust in house	**KJ409884**	**KM035031**	**KM035120**	**KM035209**
	DAOM 242697	Dust in house	**KJ409886**	**KM035033**	**KM035122**	**KM035211**
	DAOM 242699	House dust	**KJ409890**	**KM035039**	**KM035128**	**KM035217**
	DAOM 242700	House dust	**KJ409892**	**KM035041**	**KM035130**	**KM035219**
	DAOM 242702	Dust in house	**KJ409887**	**KM035034**	**KM035123**	**KM035212**
	DAOM 242704	House dust	**KJ409894**	**KM035043**	**KM035132**	**KM035221**
	DAOM 242800	Dust in house	**KJ409885**	**KM035032**	**KM035121**	**KM035210**
	MUCL 45614	Flower of unidentified angiosperm	**KJ494626**	**KM196442**	**KM196343**	**KM196396**
W. canadensis	**DAOM 226642**	Indoor of residence	**KJ409879**	**KM035025**	**KM035114**	**KM035203**
	DAOM 242570	Indoor environment	**KJ409918**	**KM035080**	**KM035169**	**KM035257**
	CBS 110622	Catwalk in silos	**AY302517**	**KM196457**	**KM196357**	**KM196407**
W. Tropicalis	**EXF-8739 T**	House dust	**KJ409878**	**KM035023**	**KM035112**	**KM035201**
	EXF-8744	House dust	**KJ409891**	**KM035040**	**KM035129**	**KM035218**
	CBS 120010	Soil	**KM217176**	**KM196470**	**KM196317**	**KM196415**

W. muriae	**CBS 136844**	Office building	**KJ409910**	**KM035064**	**KM035153**	**KM035241**
	EXF-3554	Saturated sugar solution	**KJ494605**	**KM196422**	**KM196328**	**KM196374**
	EXF-4967	Hypersaline water of Dead Sea	**KJ494610**	**KM196423**	**KM196329**	**KM196375**
	EXF-5678	Halophyte	**KJ494603**	**KM196426**	**KM196332**	**KM196379**
	EXF-5681	Halophyte	**KJ494600**	**KM196427**	**KM196333**	**KM196380**
	EXF-5685	Halophyte	**KJ494601**	**KM196428**	**KM196334**	**KM196381**
	EXF-5915	Living room wall	**KJ494593**	**KM035091**	**KM035180**	**KM035266**
	EXF-5916	Kitchen wall	**KJ494594**	**KM035090**	**KM035179**	**KM035265**

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